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FT      /label= Signature_sequence
FT      Modified-site 535
FT      /note= "Potential phosphorylation site"
FT      Modified-site 536
FT      /note= "Potential phosphorylation site"
XX      MO9958558-A2.
XX      18-NOV-1999.
XX      13-MAY-1999; 99WO-US010567.
XX      13-MAY-1998; 98US-0085343P.
XX      26-AUG-1998; 98US-0098010P.
XX      (INCY-) INCYTE PHARM INC.
XX      Bandman O, Hillman JL, Lal P, Yue H, Tang YT, Patterson C,
XX      Baughn MR, Yang J;
XX      WPI: 2000-086432/07.
XX      N-PSDB; AAA29233.
XX      Human cell signaling proteins useful for, e.g. diagnosing cell
XX      proliferative and inflammatory disorders.
XX      Claim 1; Page 77-78; 90pp; English.
XX      The present sequence is cell signaling protein-12 (CSIGP-12) encoded by
XX      cDNA obtained from Incyte clone 3293149 of COLAUCT01 library. It is
XX      expressed in musculoskeletal, gastrointestinal and nervous tissues and is
XX      found to be homologous to beta-transducin repeats containing protein.
XX      Fragments of CSIGP encoding nucleic acid can be used as hybridisation
XX      probe for detecting CSIGP related sequences or allelic variants.
XX      Recombinant CSIGP can be produced in host cells by transforming them with
XX      genetically engineered vectors. Agonists or antagonists can be used in
XX      the treatment of cell proliferative and inflammatory disorders associated
XX      with decreased or increased CSIGP expression. CSIGP is used in the
XX      diagnosis, prevention and treatment of cell proliferative disorders like
XX      arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders
XX      like AIDS, Addison's disease, multiple sclerosis, etc
XX      Sequence 569 AA;
XX      Query Match 100.0%; Score 3034; DB 3; Length 569;
XX      Best Local Similarity 100.0%; Pred. No. 7.4e-286;
XX      Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MPAEAVLQERALKFNNSSEREDCNNGEPKRIPEKNSLRQTVNSCARLCINQETVCLA 60
DB      1 MPAEAVLQERALKFNNSSEREDCNNGEPKRIPEKNSLRQTVNSCARLCINQETVCLA 60
QY      61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYPEQWSESQVEFVEHL 120
DB      61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYPEQWSESQVEFVEHL 120
QY      121 ISQMGCHYGHGHTNSYKPMLOQDFITALLPARGLDHTAENITSLYLDAKSCIAAEVLCKEWMY 180
DB      121 ISQMGCHYGHGHTNSYKPMLOQDFITALLPARGLDHTAENITSLYLDAKSCIAAEVLCKEWMY 180
QY      181 RYTSQGMMLKLLIERNVRTDSLWRGLAERRGNGOYLFKNKPPDGNAPPSFPRALYPKTI 240
DB      181 RYTSQGMMLKLLIERNVRTDSLWRGLAERRGNGOYLFKNKPPDGNAPPSFPRALYPKTI 240
QY      241 QDIETIESNMRGSRSLQRIHCRSETSKGVCLQYDDQKIVSGLRDNITIKIMDKNTLECK 300
DB      241 QDIETIESNMRGSRSLQRIHCRSETSKGVCLQYDDQKIVSGLRDNITIKIMDKNTLECK 300
QY      301 RILTGHTGVLCLQYDERVIITIGSSSDSTYRWVDVNTGEMLNTLIHHCENVLHLRFNNGMM 360
DB      301 RILTGHTGVLCLQYDERVIITIGSSSDSTYRWVDVNTGEMLNTLIHHCENVLHLRFNNGMM 360
QY      361 VTCSKDRSLAVWDMASPTDITLRRVLVGRRAVNVVDPDDKYIVSASGRTIKWMTSTNC 420

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DB      361 VTCSKDRSLAVWDMASPTDITLRRVLVGRRAVNVVDPDDKYIVSASGRTIKWMTSTNC 420
QY      421 EFVRTLNGHKRGIACTQYRDRLVSGSSDNTIRLMDIEGACRLVLEGHEELVRCIRPN 480
DB      421 EFVRTLNGHKRGIACTQYRDRLVSGSSDNTIRLMDIEGACRLVLEGHEELVRCIRPN 480
QY      481 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRLTVHSGRVFRLOPQFQVSSSHDT 540
DB      481 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRLTVHSGRVFRLOPQFQVSSSHDT 540
QY      541 ILIWFPLNDPAAQAEPSPSRRTYTYISR 569
DB      541 ILIWFPLNDPAAQAEPSPSRRTYTYISR 569
XX      RESULT 3
XX      AAB12813
XX      ID AAB12813 standard; protein; 569 AA.
XX      AC AAB12813;
XX      DT 27-NOV-2000 (first entry)
XX      DE Human beta-transducin repeat containing protein (beta-Trcp) SEQ ID NO:3.
XX      KW Ubiquitin ligase SCF complex; F-box protein; ubiquitination; Ikappab;
XX      beta-catenin; Skp1; Cull; F-box motif; WD40 repeat motif; FMD1;
XX      beta-Trcp; colon cancer; beta-transducin repeat containing protein;
XX      beta-Trcp.
XX      OS Homo sapiens.
XX      PN JP2000166542-A.
XX      PD 20-JUN-2000.
XX      PF 02-DEC-1998; 98JP-00343437.
XX      PR 02-DEC-1998; 98JP-00343437.
XX      PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX      DR WPI: 2000-485550/43.
XX      DR N-PSDB; AAA73132.
XX      PT F-box protein of ubiquitin ligase SCF complex which promotes the
XX      ubiquitination of Ikappab or beta-catenin.
XX      PS Claim 3; Page 10-12; 19pp; Japanese.
XX      The present invention describes an F-box motif protein of ubiquitin
XX      ligase SCF complex which promotes the ubiquitination of Ikappab or beta-
XX      catenin and is constituted by Skp1 protein, Cull protein and a complex
XX      (SCF complex) of F-box protein containing F-box motif and WD40 repeat
XX      motif and has the amino acid sequence of 45 residues (AAB12811) or one of
XX      two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FMD1
XX      protein) and (AAB12813, which is human beta-transducin repeat containing
XX      protein (beta-Trcp)). The F-box protein can be used for the gene therapy
XX      of colon cancer by being recombined to a virus vector
XX      Sequence 569 AA;
XX      Query Match 100.0%; Score 3034; DB 3; Length 569;
XX      Best Local Similarity 100.0%; Pred. No. 7.4e-286;
XX      Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MPAEAVLQERALKFNNSSEREDCNNGEPKRIPEKNSLRQTVNSCARLCINQETVCLA 60
DB      1 MPAEAVLQERALKFNNSSEREDCNNGEPKRIPEKNSLRQTVNSCARLCINQETVCLA 60
QY      61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYPEQWSESQVEFVEHL 120

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Db 61 STAMKTENCVAKTKYLANGTSSWIVPKORKLSASYEKEKELCVKPEQMSSEDOVEFEVHLL 120
QY 121 ISOMCHYOHGHINSYLYKPMLOQDFITLALPARGLDHIENIISYLDASLSLCAAEIVCKEMW 180
Db 121 ISOMCHYOHGHINSYLYKPMLOQDFITLALPARGLDHIENIISYLDASLSLCAAEIVCKEMW 180
QY 181 RVTSDGMLMKKLIBMVRTDSLWRGLAERBGWGYLFKNKPPDGNAPNSFYRALYPKII 240
Db 181 RVTSDGMLMKKLIBMVRTDSLWRGLAERBGWGYLFKNKPPDGNAPNSFYRALYPKII 240
QY 241 QDIETIESNMRGSHSLORHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
Db 241 QDIETIESNMRGSHSLORHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
QY 301 RILVHTGTSVCLQYDERVIITGSSDSTVRVWVNTGEMLNTLHHCEAVLHLRPNNGM 360
Db 301 RILVHTGTSVCLQYDERVIITGSSDSTVRVWVNTGEMLNTLHHCEAVLHLRPNNGM 360
QY 361 VTCSKDRSIAVWDMASPTDITLRLVYVGHRAAVNVVDFDKYIVSASGDRITKWNSTC 420
Db 361 VTCSKDRSIAVWDMASPTDITLRLVYVGHRAAVNVVDFDKYIVSASGDRITKWNSTC 420
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Db 421 EFVRTLNGHKRGIACTQYRDLRVVSGSSDNTIRLMDIECGACLRVLEGBHELVRCIRPDN 480
QY 481 KRIVSGAIVDGKIKWMDLVAAALDPRAPAGTLCIRTIVHSGRVRLQDFEFOIVSSSHDT 540
Db 481 KRIVSGAIVDGKIKWMDLVAAALDPRAPAGTLCIRTIVHSGRVRLQDFEFOIVSSSHDT 540
QY 541 ILIWFPLNDPAAQAEPSPSPRTTYISR 569
Db 541 ILIWFPLNDPAAQAEPSPSPRTTYISR 569

RESULT 4

AA96697
ID AA96697 standard; protein; 569 AA.

AC AA96697;

DT 26-SEP-2000 (first entry)

DE Human beta-TTCP.

KA E3 ubiquitin ligase; beta-TTCP; F-box; WD protein; I-kappa-B; inhibitor;
KW nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral;
KW anti-inflammatory; immunosuppressive; cyostatic.

OS Homo sapiens.

PN WO200034447-A2.

PD 15-JUN-2000.

PF 09-DEC-1999; 99WO-US029371.

PR 10-DEC-1998; 98US-00210060.

PA (SIGNS) SIGNAL PHARM INC.
PA (YISS) YISSUM RES & DEV CO.

PI Manning AM, Mercurio F, Amit S, Ben-Neriah Y, Davis M,
PI Hatzuda A, Lavon I, Yaron A;

DR WPI; 2000-431294/37.

DR N-PSDB; AAA51229.

PT Polypeptide enhancing phosphorylated I-kappa-B ubiquitination useful for
PT treating disorder associated with NF-kappa-B activation e.g. cancer,
PT comprising amino acid sequence of human E3 ubiquitin ligase or its
PT variant.

PS Claim 21; Page 72-74; 77pp; English.
CC Human beta-TTCP, an F-box/WD protein family member, has been shown to
CC have homology to human E3 ubiquitin ligase (E3). E3 enhances
CC ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of
CC nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B degradation
CC via the ubiquitin pathway is useful for identifying modulators of this
CC process for use in treating diseases associated with activation of NF-
CC kappa-B. In vitro analysis suggests that deletion of the F-box results in
CC a protein that functions as a dominant negative molecule in vivo.
CC Transient over-expression of delta-beta-TTCP (a deletion mutant)
CC inhibited the degradation of endogenous I-kappa-B-alpha in stimulated
CC Jurkat cells, resulting in accumulation of phosphorylated I-kappa-B-
CC alpha. E3 can be used to screen for modulators of NF-kappa-B activity. E3
CC and beta-TTCP can be used to modulate NF-kappa-B to treat inflammatory
CC diseases, autoimmune diseases, cancer and viral infections
SQ Sequence 569 AA;

Query Match 100.0%; Score 3034; DB 3; Length 569;
Best Local Similarity 100.0%; Pred. No. 7.4e-286;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFMSNRRDCNNGEPKIIPEKNSLRQYNSCARLCLNGETVCLA 60
Db 1 MDPAAVLQEKALKFMSNRRDCNNGEPKIIPEKNSLRQYNSCARLCLNGETVCLA 60

QY 61 STAMKTENCVAKTKYLANGTSSWIVPKORKLSASYEKEKELCVKPEQMSSEDOVEFEVHLL 120

Db 61 STAMKTENCVAKTKYLANGTSSWIVPKORKLSASYEKEKELCVKPEQMSSEDOVEFEVHLL 120

QY 121 ISOMCHYOHGHINSYLYKPMLOQDFITLALPARGLDHIENIISYLDASLSLCAAEIVCKEMW 180

Db 121 ISOMCHYOHGHINSYLYKPMLOQDFITLALPARGLDHIENIISYLDASLSLCAAEIVCKEMW 180

QY 181 RVTSDGMLMKKLIBMVRTDSLWRGLAERBGWGYLFKNKPPDGNAPNSFYRALYPKII 240

Db 181 RVTSDGMLMKKLIBMVRTDSLWRGLAERBGWGYLFKNKPPDGNAPNSFYRALYPKII 240

QY 241 QDIETIESNMRGSHSLORHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300

Db 241 QDIETIESNMRGSHSLORHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300

QY 301 RILVHTGTSVCLQYDERVIITGSSDSTVRVWVNTGEMLNTLHHCEAVLHLRPNNGM 360

Db 301 RILVHTGTSVCLQYDERVIITGSSDSTVRVWVNTGEMLNTLHHCEAVLHLRPNNGM 360

QY 361 VTCSKDRSIAVWDMASPTDITLRLVYVGHRAAVNVVDFDKYIVSASGDRITKWNSTC 420

Db 361 VTCSKDRSIAVWDMASPTDITLRLVYVGHRAAVNVVDFDKYIVSASGDRITKWNSTC 420

QY 421 EFVRTLNGHKRGIACTQYRDLRVVSGSSDNTIRLMDIECGACLRVLEGBHELVRCIRPDN 480

Db 421 EFVRTLNGHKRGIACTQYRDLRVVSGSSDNTIRLMDIECGACLRVLEGBHELVRCIRPDN 480

QY 481 KRIVSGAIVDGKIKWMDLVAAALDPRAPAGTLCIRTIVHSGRVRLQDFEFOIVSSSHDT 540

Db 481 KRIVSGAIVDGKIKWMDLVAAALDPRAPAGTLCIRTIVHSGRVRLQDFEFOIVSSSHDT 540

QY 541 ILIWFPLNDPAAQAEPSPSPRTTYISR 569

Db 541 ILIWFPLNDPAAQAEPSPSPRTTYISR 569

RESULT 5

AA983250
ID AA983250 standard; protein; 569 AA.

AC AA983250;

DT 16-AUG-2000 (first entry)

DE F-box protein hbetatTcP.

XX Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilization; proteolysis; drug discovery; gene therapy; cancer;
 KM oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KM human.
 XX Homo sapiens.
 OS
 XX MO200022110-A2.
 PN
 XX 20-APR-2000.
 PD
 XX 08-OCT-1999; 99WO-US023705.
 PF
 XX 09-OCT-1998; 98US-0103787P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Zhou P, Howley P;
 PI
 XX WPI: 2000-317970/27.
 DR
 XX N-PSDB; AA293710.
 PT Targeting degradation of polypeptide useful for treating cancer and other
 PT proliferative disorders, involves conjugating polypeptide with ubiquitin
 PT protein ligase or inhibiting ubiquitination using organic compound.
 XX
 PS Claim 9, Page 171, 185pp; English.
 CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing the
 CC ubiquitin ligase in a cell linked to the interaction domain of the target
 CC polypeptide and thereby recruiting the target polypeptide to the
 CC ubiquitin ligase. Such methods are useful for decreasing or increasing
 CC the level of a target polypeptide and for creating and expressing a
 CC destabilized polypeptide which is subjected to SCF mediated proteolysis.
 CC degrading any desired protein in a cell is useful for preventing or
 CC treating diseases caused by the presence of abnormal amount of the
 CC specific polypeptides, for drug discovery and for gene therapy. Diseases
 CC treated include cancer, by degradation of oncoproteins, Huntington's
 CC disease, other proliferative disorders and microbial infections. The
 CC method provides a quick and easy alternative to gene knockout technology.
 CC The target polypeptide can be degraded at all stages, or a specific
 CC stage, of development in the mature animal
 XX
 XX Sequence 569 AA;
 SQ

Query Match 100.0%; Score 3034; DB 3; Length 569;
 Best Local Similarity 100.0%; Pred. No. 7, 4e-286;
 Matches 569; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALFKPNSSEKEDCNNGEPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
 DB 1 MDPAAVLQEKALFKPNSSEKEDCNNGEPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
 QY 61 STAMTEKNCVAKTKYLANGSSMTIVPKORLSASYEKKEKLCVKYEQWSESQVAFVEHL 120
 DB 61 STAMTEKNCVAKTKYLANGSSMTIVPKORLSASYEKKEKLCVKYEQWSESQVAFVEHL 120
 QY 121 ISOMCHYGHGINSYLYKPMLOPDTALPARGLDIAENITSLYDLAKSLCAELVCKEWMY 180
 DB 121 ISOMCHYGHGINSYLYKPMLOPDTALPARGLDIAENITSLYDLAKSLCAELVCKEWMY 180
 QY 181 RYTSQGMILMKKLIEMVWRTDSLWRGLAERGGQYLFKNKPPDGNAPNSFYRALYPKII 240
 DB 181 RYTSQGMILMKKLIEMVWRTDSLWRGLAERGGQYLFKNKPPDGNAPNSFYRALYPKII 240
 QY 241 ODIEETESNMRGSRSLORIRHCRSETSKGVYCLQYDDOKYVGLADNTIKIMDKNTLBEK 300
 DB 241 ODIEETESNMRGSRSLORIRHCRSETSKGVYCLQYDDOKYVGLADNTIKIMDKNTLBEK 300
 QY 301 RLITGHTGSVLCLOQDERVILITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGWM 360

DB 301 RLITGHTGSVLCLOQDERVILITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGWM 360
 QY 361 VTCSKDRSLAVWDMASPDITLRRLVVGHRAAVNVVDFPDKTYVSAAGRTTKWNTSTC 420
 DB 361 VTCSKDRSLAVWDMASPDITLRRLVVGHRAAVNVVDFPDKTYVSAAGRTTKWNTSTC 420
 QY 421 EFVRTLNGHKGRIACLOQRDRRLVSGSSDNTRLMDIEGACLRVLEGHEELVRCIRFDN 480
 DB 421 EFVRTLNGHKGRIACLOQRDRRLVSGSSDNTRLMDIEGACLRVLEGHEELVRCIRFDN 480
 QY 481 KRIVSGAYDGKIKWMDLVAAALDPRAAPAGTLCLRTLVHSGRVRLQDFEQIVSSSHDT 540
 DB 481 KRIVSGAYDGKIKWMDLVAAALDPRAAPAGTLCLRTLVHSGRVRLQDFEQIVSSSHDT 540
 QY 541 IILWDFLNDPAAQAEPSPRSRTTYISR 569
 DB 541 IILWDFLNDPAAQAEPSPRSRTTYISR 569

RESULT 6
 ID AAY83041 standard; protein; 569 AA.
 AC AAY83041;
 DT 16-AUG-2000 (first entry)
 DE F-box protein FBP-1.
 KW F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
 KW proliferative disorder; differentiative disorder; breast cancer;
 KW prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
 KW immune disorder; cardiovascular disorder; inflammatory disorder; human.
 OS Homo sapiens.
 PN MO200012679-A1.
 PD 09-MAR-2000.
 PF 27-AUG-1999; 99WO-US019560.
 PR 28-AUG-1998; 98US-0098355P.
 PR 03-FEB-1999; 99US-0118568P.
 PR 15-MAR-1999; 99US-012449P.
 PA (UYNV) UNIV NEW YORK STATE.
 PI Chisaur DS, Pagano M, Latres E;
 DR WPI: 2000-256635/22.
 DR N-PSDB; AA293350.
 PT Novel nucleic acid for screening compounds useful for treating
 PT proliferative and differentiative disorders such as cancer and immune
 PT disorders comprises sequences encoding ubiquitin ligases.
 PS Disclosure; Fig 3a; 245pp; English.
 CC Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases
 CC with F-box motifs (F-box proteins) are useful for diagnosis of
 CC proliferative and differentiated related disorders by measuring FBP gene
 CC expression. Cells expressing such proteins or their fragments are useful
 CC for screening compounds. The compounds are agonists or antagonists, which
 CC are useful for treating a proliferative or differentiative disorder in a
 CC mammal such as breast, ovarian and prostate cancer and small cell lung
 CC carcinoma and also major opportunistic infections, immune disorders,
 CC cardiovascular diseases and inflammatory disorders. FBP protein, analogs,
 CC derivatives and their subsequences, anti-FBP antibodies are also useful
 CC in diagnosis of the disorders
 XX
 XX Sequence 569 AA;
 SQ

Query Match 100.0%; Score 3034; DB 3; Length 569;
 Best Local Similarity 100.0%; Pred. No. 7,4e-286;
 Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPBAVLQEKALKFNMSEREDCNGGPPPKIPEKNSLRQTVNSCARLCLINQETVCLA 60
 DB 1 MDPBAVLQEKALKFNMSEREDCNGGPPPKIPEKNSLRQTVNSCARLCLINQETVCLA 60
 QY 61 STAMKTENCVAKTKLANGTSSMIVKORKLASYEKEKELCVKYEQWSESQVEFVEHL 120
 DB 61 STAMKTENCVAKTKLANGTSSMIVKORKLASYEKEKELCVKYEQWSESQVEFVEHL 120
 QY 121 ISOMCHYOHGHINSYLPKMLQORDFTLALPARGLDHAENILSYLDASLCAAEIVCKEM 180
 DB 121 ISOMCHYOHGHINSYLPKMLQORDFTLALPARGLDHAENILSYLDASLCAAEIVCKEM 180
 QY 181 RVTSDGMLMKLIERMVRTSLMRGLAERGMGOYLFKNKPPDGNAPNPSFYRALYPKII 240
 DB 181 RVTSDGMLMKLIERMVRTSLMRGLAERGMGOYLFKNKPPDGNAPNPSFYRALYPKII 240
 QY 241 QDIETIESNMRCGRHSLORIHCRSETSKGVYCLQYDDOKIVSGLDNTIKIMDKNTLECK 300
 DB 241 QDIETIESNMRCGRHSLORIHCRSETSKGVYCLQYDDOKIVSGLDNTIKIMDKNTLECK 300
 QY 301 RILTGHTGSVLCLOYDERVIITGSSDSTVRWVNTGEMLNTLIHCEAVLHLRPNNGMM 360
 DB 301 RILTGHTGSVLCLOYDERVIITGSSDSTVRWVNTGEMLNTLIHCEAVLHLRPNNGMM 360
 QY 361 VTCSKDRSIAVMDASPTDITLRLVGLVGHRAAVVVPDDKXIYASAGDRITIKWNTSTC 420
 DB 361 VTCSKDRSIAVMDASPTDITLRLVGLVGHRAAVVVPDDKXIYASAGDRITIKWNTSTC 420
 QY 421 EFRVTLNGHKGKGIACLOYRDLVVGSSDNTIRLMDIECGACLRVLEGHEELVRCIRPDN 480
 DB 421 EFRVTLNGHKGKGIACLOYRDLVVGSSDNTIRLMDIECGACLRVLEGHEELVRCIRPDN 480
 QY 481 KRIVGAYDGKIKWMDLVAALDPRAPAGTLCRTLVEHSGRVRLOPDEFOIVSSSHDT 540
 DB 481 KRIVGAYDGKIKWMDLVAALDPRAPAGTLCRTLVEHSGRVRLOPDEFOIVSSSHDT 540
 QY 541 ILIWDPLNDPAAQAEPSPSRRTYIYSR 569
 DB 541 ILIWDPLNDPAAQAEPSPSRRTYIYSR 569

RESULT 7
 ABG69473
 ID ABG69473 standard; protein; 569 AA.
 AC ABG69473;
 DT 21-OCT-2002 (first entry)
 XX
 DE Human bait protein beta-Trcp1.
 XX Human; yeast two-hybrid assay; adipocyte; bait protein; NIDDM;
 KM non-insulin diabetes mellitus; obesity; selected interacting domain; STD;
 XX protein-protein interaction map; PIM; anorectic; metabolic disorder.
 OS Homo sapiens.
 PN W0200253726-A2.
 PD 11-JUL-2002.
 PF 28-DEC-2001; 2001WO-EP015423.
 PR 02-JAN-2001; 2001US-0259377P.
 PA (HYBR-) HYBRIGENICS.
 XX (CNRS) CENT NAT RECH SCI.
 XX

PI Legrain P, Marullo S, Jockers R;
 XX WPI; 2002-583612/62.
 DR N-PSDB; ABS51009.
 XX
 PT Novel complex of protein-protein interactions in adipocyte cells for
 PT identifying compounds that modulate the protein-protein interactions and
 PT useful for treating obesity and metabolic disorders.
 XX
 PS Claim 1; Page: 125pp; English.
 XX
 CC The invention relates to a complex of protein-protein interactions
 CC (forming a protein-protein interaction map, PIM) in adipocyte cells as
 CC defined in the specification, or polynucleotides in adipocytes encoding
 CC for the polypeptides. Also included are a recombinant cell expressing the
 CC interacting polypeptides and a method of selecting a modulating compound
 CC in adipocyte cells, by cultivating a recombinant host cell on a selective
 CC medium containing a modulating compound and a reporter gene the
 CC expression of which is toxic for the recombinant host cell which is
 CC transformed with two vectors, where the first vector comprises a
 CC polynucleotide encoding a first hybrid polypeptide and DNA binding domain
 CC and the second vector comprising a polynucleotide encoding a second
 CC hybrid polypeptide and an activating domain that activates the toxic
 CC reporter gene, when the first and second hybrid polypeptides interact and
 CC selecting the modulating compound which inhibits the growth of the
 CC recombinant host cell (i.e. using the yeast two-hybrid system). The
 CC complexes are useful for identifying compounds that modulate the protein-
 CC protein interactions and useful for treating obesity and metabolic
 CC disorders e.g. non-insulin dependent diabetes mellitus, NIDDM. The
 CC compound isolated by the method is useful for treating and preventing of
 CC obesity or metabolic diseases. The interactions between the proteins of
 CC the complex further define a set of selected interacting domains, STD.
 CC The present sequence represents a member of the protein complex of the
 CC invention, used as the bait protein in the yeast two-hybrid assay. Note:
 CC The present sequence was not displayed in the specification but was
 CC obtained from its Genbank entry by the indexer
 XX
 SQ Sequence 569 AA;

Query Match 100.0%; Score 3034; DB 5; Length 569;
 Best Local Similarity 100.0%; Pred. No. 7,4e-286;
 Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPBAVLQEKALKFNMSEREDCNGGPPPKIPEKNSLRQTVNSCARLCLINQETVCLA 60
 DB 1 MDPBAVLQEKALKFNMSEREDCNGGPPPKIPEKNSLRQTVNSCARLCLINQETVCLA 60
 QY 61 STAMKTENCVAKTKLANGTSSMIVKORKLASYEKEKELCVKYEQWSESQVEFVEHL 120
 DB 61 STAMKTENCVAKTKLANGTSSMIVKORKLASYEKEKELCVKYEQWSESQVEFVEHL 120
 QY 121 ISOMCHYOHGHINSYLPKMLQORDFTLALPARGLDHAENILSYLDASLCAAEIVCKEM 180
 DB 121 ISOMCHYOHGHINSYLPKMLQORDFTLALPARGLDHAENILSYLDASLCAAEIVCKEM 180
 QY 181 RVTSDGMLMKLIERMVRTSLMRGLAERGMGOYLFKNKPPDGNAPNPSFYRALYPKII 240
 DB 181 RVTSDGMLMKLIERMVRTSLMRGLAERGMGOYLFKNKPPDGNAPNPSFYRALYPKII 240
 QY 241 QDIETIESNMRCGRHSLORIHCRSETSKGVYCLQYDDOKIVSGLDNTIKIMDKNTLECK 300
 DB 241 QDIETIESNMRCGRHSLORIHCRSETSKGVYCLQYDDOKIVSGLDNTIKIMDKNTLECK 300
 QY 301 RILTGHTGSVLCLOYDERVIITGSSDSTVRWVNTGEMLNTLIHCEAVLHLRPNNGMM 360
 DB 301 RILTGHTGSVLCLOYDERVIITGSSDSTVRWVNTGEMLNTLIHCEAVLHLRPNNGMM 360
 QY 361 VTCSKDRSIAVMDASPTDITLRLVGLVGHRAAVVVPDDKXIYASAGDRITIKWNTSTC 420
 DB 361 VTCSKDRSIAVMDASPTDITLRLVGLVGHRAAVVVPDDKXIYASAGDRITIKWNTSTC 420
 QY 421 EFRVTLNGHKGKGIACLOYRDLVVGSSDNTIRLMDIECGACLRVLEGHEELVRCIRPDN 480
 DB 421 EFRVTLNGHKGKGIACLOYRDLVVGSSDNTIRLMDIECGACLRVLEGHEELVRCIRPDN 480

Db 421 EFVRTLNHGKGIACLOVRDLVVGSSDNTIRLMDIECGACLRVLEGEHELVR CIRFDN 480
 QY 481 KRIVGAYDGKIKWMDLVAAALDPRAAGTLCRTLVESGVRFRLOPDEFOIVSSSHDT 540
 Db 481 KRIVGAYDGKIKWMDLVAAALDPRAAGTLCRTLVESGVRFRLOPDEFOIVSSSHDT 540
 QY 541 ILIWFNDPAAQAEPSPRSRTTYTISR 569
 Db 541 ILIWFNDPAAQAEPSPRSRTTYTISR 569
 RESULT 8
 ID AAO22446 standard; protein; 569 AA.
 AC AAO22446;
 DT 11-OCT-2002 (first entry)
 DE Human F-box protein FBP1 SEQ ID No 2.
 XX
 XX Cytostatic; immunomodulator; cardiant; antiinflammatory; antimicrobial;
 KM proliferative; differentiative disorder; Skp2; F-box protein; cancer;
 KM ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer;
 KM small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP;
 KM inflammatory disorder; lymphoma; major opportunistic infection;
 KM certain cardiovascular disease; human.
 XX
 OS Homo sapiens.
 PN WO200255665-A2.
 PD 18-JUL-2002.
 XX
 PF 07-JAN-2002; 2002WO-US000311.
 XX
 PR 05-JAN-2001; 2001US-0260179P.
 XX
 PA (UNIV) UNIV NEW YORK STATE.
 XX
 PI Pagano M;
 DR WPI; 2002-599665/64.
 DR N-PSDB; AAL41041.
 XX
 PT Screening compounds for treating proliferative disorders, e.g. breast
 PT cancer or prostate cancer, infections or immune disorders, comprises
 PT detecting a change in the activity of Skp2 with either p27 or Cks1.
 XX
 PS Disclosure; Fig 3; 246pp; English.
 XX
 CC The invention relates to screening compounds useful for the treatment of
 CC proliferative or differentiative disorders comprising detecting a change
 CC in the activity of Skp2 (F-box protein). The method is useful for
 CC screening compounds for the treatment of proliferative or differentiative
 CC disorders, particularly cancer. These compounds include small molecules,
 CC or compounds or derivatives or analogues of the new ubiquitin ligases.
 CC The compounds are useful for treating diseases such as cancer (e.g.
 CC breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell
 CC lung carcinoma or parathyroid adenomas), major opportunistic infections,
 CC immune disorders, certain cardiovascular diseases or inflammatory
 CC disorders. This sequence represents an F-box protein (FBP) relating to
 CC the invention
 XX
 SQ Sequence 569 AA;
 Query Match 100.0%; Score 3034; DB 5; Length 569;
 Best Local Similarity 100.0%; Pred. No 7.4e-266;
 Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 STAMKENCVAKTKLANGTSSMIVPKORKLSASVEKEKELCVKYPEOMSESPOVEVEHL 120
 Db 61 STAMKENCVAKTKLANGTSSMIVPKORKLSASVEKEKELCVKYPEOMSESPOVEVEHL 120
 QY 121 ISOMCHYOHGHINSYLYKPMLOPFTALPARGLDHIAENIISLYDPAKSLCAAEIVCKEY 180
 Db 121 ISOMCHYOHGHINSYLYKPMLOPFTALPARGLDHIAENIISLYDPAKSLCAAEIVCKEY 180
 QY 181 RYTSDDMLMKKLIEMRVRTDSIMRGLAERRGQYLFNNKPPDGNAPPNSFYRALYPKII 240
 Db 181 RYTSDDMLMKKLIEMRVRTDSIMRGLAERRGQYLFNNKPPDGNAPPNSFYRALYPKII 240
 QY 241 ODIEETIESNRCGRSLQRHCRSTSGVYCLQYDDQKIVSGLDNNTIKIWDKNTLECK 300
 Db 241 ODIEETIESNRCGRSLQRHCRSTSGVYCLQYDDQKIVSGLDNNTIKIWDKNTLECK 300
 QY 301 RILTGHTGSVLCLOYDERVIIITGSSDSIVRVWDVNTGEMLNTLIHCEAVLHLRFNNGM 360
 Db 301 RILTGHTGSVLCLOYDERVIIITGSSDSIVRVWDVNTGEMLNTLIHCEAVLHLRFNNGM 360
 QY 361 VTCSKORSIAVWDMASPTDITLRVLYVGHRAAVNVDPDDKXIYASAGDRITKWNSTGC 420
 Db 361 VTCSKORSIAVWDMASPTDITLRVLYVGHRAAVNVDPDDKXIYASAGDRITKWNSTGC 420
 QY 421 EFVRTLNHGKGIACLOVRDLVVGSSDNTIRLMDIECGACLRVLEGEHELVR CIRFDN 480
 Db 421 EFVRTLNHGKGIACLOVRDLVVGSSDNTIRLMDIECGACLRVLEGEHELVR CIRFDN 480
 QY 481 KRIVGAYDGKIKWMDLVAAALDPRAAGTLCRTLVESGVRFRLOPDEFOIVSSSHDT 540
 Db 481 KRIVGAYDGKIKWMDLVAAALDPRAAGTLCRTLVESGVRFRLOPDEFOIVSSSHDT 540
 QY 541 ILIWFNDPAAQAEPSPRSRTTYTISR 569
 Db 541 ILIWFNDPAAQAEPSPRSRTTYTISR 569
 RESULT 9
 ID ADS88273 standard; protein; 569 AA.
 AC ADS88273;
 DT 18-NOV-2004 (first entry)
 DE Human protein of a TNF-alpha signalling pathway protein complex Seq 128.
 XX
 XX
 KM protein complex; tumour necrosis factor-alpha signalling pathway;
 KM TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
 KM inflammatory bowel disease; infectious disease; septic shock;
 KM bacterial infection; neurological disease; stroke-induced inflammation;
 KM neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
 KM antirheumatic; cytostatic; antibacterial; gene therapy; human.
 OS Homo sapiens.
 PN WO2004035783-A2.
 PD 29-APR-2004.
 XX
 PF 24-SEP-2003; 2003WO-EP050655.
 XX
 PR 26-SEP-2002; 2002EP-00021809.
 PR 10-FEB-2003; 2003EP-00100274.
 XX
 PA (CELL-) CELLZOME AG.
 XX
 PI Bouwmeester T, Huber B, Bauch A, Ruffner H, Bauer A, Kuester B,
 PI Superti-Furga G, Kruse U;
 DR WPI; 2004-348460/32.
 XX

PT New protein complex comprising at least one first and second protein of
PT the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for
PT diagnosing or treating inflammation, neurological diseases, infectious
PT diseases or cancer.

XX Example; SEQ ID NO 128; 1980bp; English.

CC This invention relates to novel protein complexes of the tumour necrosis
CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
CC methods for preparing these complexes comprising at least two component
CC proteins, as well as screening methods to identify modulators of the
CC pathway, which include antibodies, agonists and antagonists thereof. The
CC present invention describes a protein complex and kit that are useful for
CC diagnosing, prognosing or treating chronic inflammatory diseases such as
CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit antiinflammatory, antiarthritic,
CC antirheumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.

XX Sequence 569 AA;

Query Match 100.0%; Score 3034; DB 8; Length 569;
Best Local Similarity 100.0%; Pred. No. 7,4e-286;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVVOEALKKFMNSSEKEDCNNGEPKRIIPKNSLRQTYNSCARLCLNGETVCLA 60
DB 1 MDPAAVVOEALKKFMNSSEKEDCNNGEPKRIIPKNSLRQTYNSCARLCLNGETVCLA 60
QY 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQWSSDQVEFVHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQWSSDQVEFVHL 120
QY 121 ISOMCHYOHGHINSYLYKPMLOQDFITLAPAGLDHIAENILSYLDASLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLYKPMLOQDFITLAPAGLDHIAENILSYLDASLCAAEIVCKEMY 180
QY 181 RYTSNGIMMKKLIEMVWRTDSIMRGLAERKMGQYLFKNKPPDGNAPNSFYRALYPKII 240
DB 181 RYTSNGIMMKKLIEMVWRTDSIMRGLAERKMGQYLFKNKPPDGNAPNSFYRALYPKII 240
QY 241 ODIEETIESNMRGSHSLORIHCRSETSKGVYCLQYDDQKIVSGLDNTIKIMDKNTLCK 300
DB 241 ODIEETIESNMRGSHSLORIHCRSETSKGVYCLQYDDQKIVSGLDNTIKIMDKNTLCK 300
QY 301 RILGHTGTSVLCLOQDERVIITGSSDSFYRVWDVNTGEMLNTLIHCEAVLHLRFNNGMM 360
DB 301 RILGHTGTSVLCLOQDERVIITGSSDSFYRVWDVNTGEMLNTLIHCEAVLHLRFNNGMM 360
QY 361 VTCSKDRSIAVWDMAFDDITLRVLYVGHRAAVNVVDPDKITYASAGDRTIKWNTSTC 420
DB 361 VTCSKDRSIAVWDMAFDDITLRVLYVGHRAAVNVVDPDKITYASAGDRTIKWNTSTC 420
QY 421 EFWRTLNGHKGIGIACLOYRDLRVVSGSSDNTIRLMDIEGACIARVLEGBEELVRCIRPDN 480
DB 421 EFWRTLNGHKGIGIACLOYRDLRVVSGSSDNTIRLMDIEGACIARVLEGBEELVRCIRPDN 480
QY 481 KRIVSAGVYDGKIKWDLVAALDPRAPAGTLCLRTLVHSGRVFRLOPDEFOQVSSSHDT 540
DB 481 KRIVSAGVYDGKIKWDLVAALDPRAPAGTLCLRTLVHSGRVFRLOPDEFOQVSSSHDT 540
QY 541 ILIWDPLNDPAAQAEPPSPSRITYIISR 569
DB 541 ILIWDPLNDPAAQAEPPSPSRITYIISR 569

RESULT 10
AAB48298
ID AAB48298 standard; protein; 569 AA.

XX AAB48298;

DT 02-APR-2001 (first entry)

DE Human ZF11 protein.

XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW Bad; Bcl-2; tumour; cytosolic.

OS Homo sapiens.

PN WO200075184-A1.

PD 14-DEC-2000.

PF 05-JUN-2000; 2000WO-US015449.

PR 04-JUN-1999; 99US-0137494P.

PA (UYUA) UNIV YALE.

PI Zhang H, Tsvetkov LM, Kondo T;

XX WPI; 2001-061703/07.

DR N-PSDB; AAC84610.

PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
PT involves altering levels of proteins such as S-phase kinase associated
PT proteins 1, 2 and cullin/CDC53 proteins.

PS Claim 3; Page 130-132; 162bp; English.

XX The invention relates to methods of altering the polypeptide levels in a
XX cell, using proteins selected from S-phase kinase associated proteins 1
XX and 2 (SKP1, SKP2), SKP2-like proteins (ZF) and CUL-1 (a member of the
XX cullin/CDC53 family of proteins). The method is useful for altering the
XX level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
XX polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
XX detecting tumours, and in monitoring tumor treatment in a mammal. Agents
XX that modulate interactions between SKP and target proteins are useful for
XX treating tumours

XX Sequence 569 AA;

Query Match 99.8%; Score 3027; DB 4; Length 569;
Best Local Similarity 99.8%; Pred. No. 3.6e-285;
Matches 568; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAAVVOEALKKFMNSSEKEDCNNGEPKRIIPKNSLRQTYNSCARLCLNGETVCLA 60
DB 1 MDPAAVVOEALKKFMNSSEKEDCNNGEPKRIIPKNSLRQTYNSCARLCLNGETVCLA 60
QY 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQWSSDQVEFVHL 120
DB 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKFEQWSSDQVEFVHL 120
QY 121 ISOMCHYOHGHINSYLYKPMLOQDFITLAPAGLDHIAENILSYLDASLCAAEIVCKEMY 180
DB 121 ISOMCHYOHGHINSYLYKPMLOQDFITLAPAGLDHIAENILSYLDASLCAAEIVCKEMY 180
QY 181 RYTSNGIMMKKLIEMVWRTDSIMRGLAERKMGQYLFKNKPPDGNAPNSFYRALYPKII 240
DB 181 RYTSNGIMMKKLIEMVWRTDSIMRGLAERKMGQYLFKNKPPDGNAPNSFYRALYPKII 240
QY 241 ODIEETIESNMRGSHSLORIHCRSETSKGVYCLQYDDQKIVSGLDNTIKIMDKNTLCK 300
DB 241 ODIEETIESNMRGSHSLORIHCRSETSKGVYCLQYDDQKIVSGLDNTIKIMDKNTLCK 300

QY 301 RILTGHTGSLVCLQYDERVIITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGM 360
| | | | |
DB 301 RILTGHTGSLVCLQYDERVIITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGM 360
QY 361 VTCSKDRSIAVMDMSPDTITLRLVVGRAAVNVDPDKYIVASGDRITIKWNTSTC 420
| | | | |
DB 361 VTCSKDRSIAVMDMSPDTITLRLVVGRAAVNVDPDKYIVASGDRITIKWNTSTC 420
QY 421 EFVRTLNGHKGIGACIQYRDLVVGSSSDNTIRLMDIEGACLRVLEGHBEIVRCIRFDN 480
| | | | |
DB 421 EFVRTLNGHKGIGACIQYRDLVVGSSSDNTIRLMDIEGACLRVLEGHBEIVRCIRFDN 480
QY 481 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRTIVHSGRVRLQDFEQIVSSSDHT 540
| | | | |
DB 481 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRTIVHSGRVRLQDFEQIVSSSDHT 540
QY 541 ILIMDFLNDPAAQAEPSPSPRTTYTISR 569
| | | | |
DB 541 ILIMDFLNDPAAQAEPSPSPRTTYTISR 569
RESULT 11
AAM00960
ID AAM00960 standard; protein; 608 AA.
AC AAM00960;
XX
DT 01-OCT-2001 (first entry)
XX
DE Human bone marrow protein, SEQ ID NO: 436.
XX
KW Human; bone marrow; antiinflammatory; cytosolic; neuroprotective;
antiviral; antibacterial; antifungal; anti-HIV; haemostatic;
immunosuppressive; gene therapy; cytokine cell proliferation;
cell differentiation modulator; immune disorder; infection; cancer;
human immunodeficiency virus; HIV; autoimmune disorder; haemophilia.
XX
OS Homo sapiens.
XX
PN WO200153453-A2.
XX
PD 26-JUL-2001.
XX
PF 23-DEC-2000; 2000WO-US034960.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 30-NOV-2000; 2000US-0250583P.
XX
XX
PA (HYSE-) HYSEQ INC.
XX
PI Ford JE, Boyle BJ, Tang YT, Liu C, Asundi V, Chen R, Ma Y,
PI Ren F, Wang J, Werhman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
PI Zhou P, Dmanac RT;
XX
DR WPI: 2001-488707/53.
XX
DR N-PSDB; AAH90079.
XX
PT Novel bone-marrow-expressed polynucleotides and polypeptides, useful for
PT treating e.g. cancer and immune deficiency disorders.
XX
PS Claim 10; Page 523-524; 648pp; English.
XX
CC The present sequence is one of 251 novel human polypeptides encoded by a
CC bone marrow-expressed polynucleotide. The polynucleotide and the
CC polypeptide encoded by it are useful in the treatment of various immune

CC deficiencies and disorders. The deficiencies and disorders may be
CC genetic, may be caused by a viral (e.g. HIV), bacterial or fungal
CC infection, or may result from an autoimmune disorder, a coagulation
CC disorder (e.g. haemophilia), inhibition of tumour cell proliferation,
CC suppression of an inflammatory response or treatment of a nervous system
CC disorder such as Alzheimer's disease. Detection of the presence or
CC increased expression of the polynucleotide or the protein it encodes is
CC useful for the diagnosis and/or prognosis of one or more types of cancer.
CC The polynucleotide and polypeptide can be used as nutritional sources or
CC supplements and in the screening of chemical compounds as potential drugs
XX
SQ Sequence 608 AA;
XX
Query Match 99.8%; Score 3027; DB 4; Length 608;
Best Local Similarity 99.6%; Pred No. 46-285;
Matches 567; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MDPAAVLAQEKALKFMSNSEREDCNNGEPKRIPEKNSLRQTVNSCARLCINQETVCLA 60
| | | | |
DB 40 MDPAAVLAQEKALKFMSNSEREDCNNGEPKRIPEKNSLRQTVNSCARLCINQETVCLA 99
QY 61 STAKTENCVAATKILANGTSSMIVPKOKLASYEKELCVKYEPQWSESQVEFEHL 120
| | | | |
DB 100 STAKTENCVAATKILANGTSSMIVPKOKLASYEKELCVKYEPQWSESQVEFEHL 159
QY 121 ISQMGHGHINSYLLKPLQDFITLPAKGLDIAENIISYLLAKSLCAAEIVCKEY 180
| | | | |
DB 160 ISQMGHGHINSYLLKPLQDFITLPAKGLDIAENIISYLLAKSLCAAEIVCKEY 219
QY 181 RYTSQGMMLKLIEMVVRTDSLRLGIAERGGQYLFKNKPPDGNAPNSFYALYPKII 240
| | | | |
DB 220 RYTSQGMMLKLIEMVVRTDSLRLGIAERGGQYLFKNKPPDGNAPNSFYALYPKII 279
QY 241 QDIETIESNWRGGRHSLOIRHCRSTSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLBECK 300
| | | | |
DB 280 QDIETIESNWRGGRHSLOIRHCRSTSGVYCLQYDDQKIVSGLRDNTIKIWDKNTLBECK 339
QY 301 RILTGHTGSLVCLQYDERVIITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGM 360
| | | | |
DB 340 RILTGHTGSLVCLQYDERVIITGSSDSTVRVMDVNTGEMLNTLIHCEAVLHLRFNNGM 399
QY 361 VTCSKDRSIAVMDMSPDTITLRLVVGRAAVNVDPDKYIVASGDRITIKWNTSTC 420
| | | | |
DB 400 VTCSKDRSIAVMDMSPDTITLRLVVGRAAVNVDPDKYIVASGDRITIKWNTSTC 459
QY 421 EFVRTLNGHKGIGACIQYRDLVVGSSSDNTIRLMDIEGACLRVLEGHBEIVRCIRFDN 480
| | | | |
DB 460 EFVRTLNGHKGIGACIQYRDLVVGSSSDNTIRLMDIEGACLRVLEGHBEIVRCIRFDN 519
QY 481 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRTIVHSGRVRLQDFEQIVSSSDHT 540
| | | | |
DB 520 KRIVSGAYDGKIKWMDLVAAALDPRAPAGTLCRTIVHSGRVRLQDFEQIVSSSDHT 579
QY 541 ILIMDFLNDPAAQAEPSPSPRTTYTISR 569
| | | | |
DB 580 ILIMDFLNDPAAQAEPSPSPRTTYTISR 608
RESULT 12
AAM78582
ID AAM78582 standard; protein; 605 AA.
AC AAM78582;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1244.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX

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OS Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX
XX 27-APR-2000; 2000US-00560875.
XX
XX 20-JUN-2000; 2000US-00598075.
XX
XX 19-JUL-2000; 2000US-00620325.
XX
XX 01-SEP-2000; 2000US-00654936.
XX
XX 15-SEP-2000; 2000US-00663561.
XX
XX 20-OCT-2000; 2000US-00693325.
XX
XX 30-NOV-2000; 2000US-00728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX
XX N-PSDB; AAK51715.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX PT in diagnosis and gene therapy.
XX
XX Claim 20; Page 3503-3504; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK51435) and the
XX CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
XX CC cytokine, cell proliferation or cell differentiation or which may induce
XX CC production of other cytokines in other cell populations. The
XX CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX CC peptide therapy. The polypeptides have various cytokine-like activities,
XX CC e.g. stem cell growth factor activity, haematopoiesis regulating
XX CC activity, tissue growth factor activity, immunomodulatory activity and
XX CC activin/inhibin activity and may be useful in the diagnosis and/or
XX CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
XX CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
XX CC sequence listing were missing at the time of publication
XX
XX Sequence 605 AA:
SQ
Query Match 99.1%; Score 3006; DB 4; Length 605;
Best Local Similarity 94.0%; Pred. No. 4,4e-283;
Matches 569; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 1 MDPAAVAVLOEKALK-----FNNSSERBDC 24
DB 1 MDPAAVAVLOEKALKMCMSPRSLWLGCSLADMSLSRLCLYNPGTALTAFFNNSSEBDC 60
QY 25 NNGEPPRKIIIPKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTCLANGSSMIV 84
DB 61 NNGEPPRKIIIPKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTCLANGSSMIV 120
QY 85 PRORKLASAYEKEKELCVKYFEQMSQSDQVEFEVHLISQMCHYQGHINSYKPMLOQDF 144
DB 121 PRORKLASAYEKEKELCVKYFEQMSQSDQVEFEVHLISQMCHYQGHINSYKPMLOQDF 180
QY 145 ITALPARGLDHTAENILSTLDAKSLCAAEIVCKEWRVYRTSDMLMKKILERRVVRTDSIMR 204
DB 161 ITALPARGLDHTAENILSTLDAKSLCAAEIVCKEWRVYRTSDMLMKKILERRVVRTDSIMR 240
QY 205 GLAERRGMOYLFKNKPPDGNAPNPSFYALYPKIIDIETIESNMWRCGRHSLQRIHCRS 264
DB 241 GLAERRGMOYLFKNKPPDGNAPNPSFYALYPKIIDIETIESNMWRCGRHSLQRIHCRS 300
QY 265 ETSKGVYCLQYDDQKIVSGLRDNTIKINDKNTLECKRIILTGHTGSVLCLQYDERVIITGS 324
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DB 301 ETSKGVYCLQYDDQKIVSGLRDNTIKINDKNTLECKRIILTGHTGSVLCLQYDERVIITGS 360
QY 325 SDSTVRVWDVNTGEMNLTLIHGCAVHLRPNNGMMVTCGKDRSIAWDMASPTDITLRR 384
DB 361 SDSTVRVWDVNTGEMNLTLIHGCAVHLRPNNGMMVTCGKDRSIAWDMASPTDITLRR 420
QY 385 VLVGHRAAVNVVDFPDXYIVSASGRTIKYWNSTCEFEVTLNGHKRGIACTQYRDLVV 444
DB 421 VLVGHRAAVNVVDFPDXYIVSASGRTIKYWNSTCEFEVTLNGHKRGIACTQYRDLVV 480
QY 445 SGSSDNTIRLMDIEGACCLVLEGESELVKCRIPDNKRIYSGAYDGKIKYWDVLAALDPR 504
DB 481 SGSSDNTIRLMDIEGACCLVLEGESELVKCRIPDNKRIYSGAYDGKIKYWDVLAALDPR 540
QY 505 APAGTLCIRTLVHSGVFRLOPDEFOIVSSSHDITLIMDFLNDPAAQAEPPRPSRTY 564
DB 541 APAGTLCIRTLVHSGVFRLOPDEFOIVSSSHDITLIMDFLNDPAAQAEPPRPSRTY 600
QY 565 TYISR 569
DB 601 TYISR 605
RESULT 13
ADS88274
ID ADS88274 standard; protein; 605 AA.
XX
XX ADS88274;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human protein of a TNF-alpha signalling pathway protein complex Seq 129.
XX
XX protein complex: tumour necrosis factor-alpha signalling pathway;
XX KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
XX KW inflammatory bowel disease; infectious disease; septic shock;
XX KW bacterial infection; neurological disease; stroke-induced inflammation;
XX KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
XX KW antirheumatic; cytostatic; antibacterial; gene therapy; human.
XX
XX OS Homo sapiens.
XX
XX WO2004035783-A2.
XX
XX 29-APR-2004.
XX
XX 24-SEP-2003; 2003WO-EP050655.
XX
XX 26-SEP-2002; 2002EP-00021809.
XX
XX 10-FEB-2003; 2003EP-00100274.
XX
XX (CELL-) CELLZOME AG.
XX
XX Bouwmeester T, Hulse B, Bauch A, Ruffner H, Bauer A, Kuester B;
XX PI Superli-Furga G, Kruse U;
XX
XX WPI; 2004-348460/32.
XX
XX New protein complex comprising at least one first and second protein of
XX PT the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for
XX PT diagnosing or treating inflammation, neurological diseases, infectious
XX PT diseases or cancer.
XX
XX Example; SEQ ID NO 129; 1980pp; English.
XX
XX This invention relates to novel protein complexes of the tumour necrosis
XX CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
XX CC methods for preparing these complexes comprising at least two component
XX CC proteins, as well as screening methods to identify modulators of the
XX CC pathway, which include antibodies, agonists and antagonists thereof. The
XX CC present invention describes a protein complex and kit that are useful for
XX CC diagnosing, prognosing or treating chronic inflammatory diseases such as
XX CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
```

CC such as septic shock and bacterial infections; neurological diseases such
CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
CC cancer. Accordingly, these complexes can be used for the development of
CC pharmaceutical compositions that exhibit anti-inflammatory, antidiabetic,
CC antineumatic, cytostatic and antibacterial activities and can be used
CC for gene therapy purposes. In particular, the invention further provides
CC siRNA-oligonucleotides useful for inhibiting protein expression for in
CC vitro or cell culture assays. This polypeptide is a human protein that
CC can be used in combination with other proteins provided in the
CC specification to form novel complexes of the TNF-alpha signalling pathway
CC of the invention.

SQ Sequence 605 AA;

Query Match 99.1%; Score 3006; DB 8; Length 605;
Best Local Similarity 94.0%; Pred. No. 4,4e-283;
Matches 569; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 1 MDPAAVLQEKALKFM-----NSSREDC 24
DB 1 MDPAAVLQEKALKFMCSMPRLIMLGCSSLADSMPLRLCLYNPGTALTAFOSSREDC 60
QY 25 NNGEPPRKIIPEKNSLRQTYNSCARLCLNOETVCLASTAMKTENCVAKTKLANGTSSMTV 84
DB 61 NNGEPPRKIIPEKNSLRQTYNSCARLCLNOETVCLASTAMKTENCVAKTKLANGTSSMTV 120
QY 85 PPKRKLASAYEKEKELCVKRYFEQWSSDOVEFEHLISQMCHYOHGHNISYKPMLOQRP 144
DB 121 PPKRKLASAYEKEKELCVKRYFEQWSSDOVEFEHLISQMCHYOHGHNISYKPMLOQRP 180
QY 145 ITALPARGDHIAENILSYLDAKSLCAELVCKEYRVTSDGMLKELIERNVTRTSLMR 204
DB 181 ITALPARGDHIAENILSYLDAKSLCAELVCKEYRVTSDGMLKELIERNVTRTSLMR 240
QY 205 GLAERRGMGOYLFPKKNPPDGNAPNSFYALYPKIIQDIETIESNMRCGRHSIORIHCRS 264
DB 241 GLAERRGMGOYLFPKKNPPDGNAPNSFYALYPKIIQDIETIESNMRCGRHSIORIHCRS 300
QY 265 ERSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECKRIITGHTGSLCLQYDERVYITGS 324
DB 301 ERSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECKRIITGHTGSLCLQYDERVYITGS 360
QY 325 SDSTVRVMDVTGEMLNTLIHCEAVLHLRFNNGMVTCSDRSIAVMMASTDTITLRR 384
DB 361 SDSTVRVMDVTGEMLNTLIHCEAVLHLRFNNGMVTCSDRSIAVMMASTDTITLRR 420
QY 385 VLVGHRAAVNVVDFDDKIYVSASGDRTIKVMNTSTCEFYRTLNGHKGRIACIQYDRLLV 444
DB 421 VLVGHRAAVNVVDFDDKIYVSASGDRTIKVMNTSTCEFYRTLNGHKGRIACIQYDRLLV 480
QY 445 SSSSNTITLMDIEGACLRVLEGEHELVRCTIRFDNKRIVSGAYDGKIRVMDLVAALDR 504
DB 481 SSSSNTITLMDIEGACLRVLEGEHELVRCTIRFDNKRIVSGAYDGKIRVMDLVAALDR 540
QY 505 APAGTLCRTLVHSGRVRFLQDFEQIVSSSHDDTITLMDFLNDPAQAABPPSPSRIT 564
DB 541 APAGTLCRTLVHSGRVRFLQDFEQIVSSSHDDTITLMDFLNDPAQAABPPSPSRIT 600
QY 565 TYISR 569
DB 601 TYISR 605

RESULT 14

ID AAB12812 standard; protein; 569 AA.

XX AAB12812;

XX 27-NOV-2000 (first entry)

XX Mouse ubiquitin ligase FWD1 protein SEQ ID NO:2.

KW Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB;
KW beta-catenin; Skp1; Cull1; F-box motif; WD40 repeat motif; FWD1;
KW gene therapy; colon cancer; beta-transducin repeat containing protein;
KW beta-Trcp.

XX Mus musculus.

PN JP2000166542-A.

PD 20-JUN-2000.

PF 02-DEC-1998; 98UP-00343437.

PR 02-DEC-1998; 98UP-00343437.

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

DR WPI; 2000-485550/43.

XX N-PSDB; AAA73131.

PT F-box protein of ubiquitin ligase SCF complex which promotes the
XX ubiquitination of IkappaB or beta-catenin.

XX Claim 2; Page 9-10; 199p; Japanese.

CC The present invention describes an F-box motif protein of ubiquitin
CC ligase SCF complex which promotes the ubiquitination of IkappaB or beta-
CC catenin and is constituted by Skp1 protein, Cull1 protein and a complex
CC (SCF complex) of F-box protein containing F-box motif and WD40 repeat
CC motif and has the amino acid sequence of 45 residues (AAB12811) or one of
CC two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1
CC protein) and (AAB12813, which is human beta-transducin repeat containing
CC protein (beta-Trcp)). The F-box protein can be used for the gene therapy
CC of colon cancer by being recombined to a virus vector

SQ Sequence 569 AA;

Query Match 98.8%; Score 2997; DB 3; Length 569;
Best Local Similarity 98.6%; Pred. No. 3e-282;
Matches 561; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFMSSEREDCNGGPPRKIIPEKNSLRQTYNSCARLCLNOETVCL 60
DB 1 MDPAAVLQEKALKFMSSEREDCNGGPPRKIIPEKNSLRQTYNSCARLCLNOETVCL 60
QY 61 STAMKTENCVAKTKLANGTSSMTIVPKORLSAYEKEKELCVKRYFEQWSSDOVEFEHL 120
DB 61 STAMKTENCVAKTKLANGTSSMTIVPKORLSAYEKEKELCVKRYFEQWSSDOVEFEHL 120
QY 121 ISQMCHYOHGHNISYKPMLOQRPFTALPARGLDHAENILSYLDAKSLCAELVCKEY 180
DB 121 ISQMCHYOHGHNISYKPMLOQRPFTALPARGLDHAENILSYLDAKSLCAELVCKEY 180
QY 181 RVTSDGMLKELIERNVTRTSLMRGLAERRGMGOYLFPKKNPPDGNAPNSFYALYPKII 240
DB 181 RVTSDGMLKELIERNVTRTSLMRGLAERRGMGOYLFPKKNPPDGNAPNSFYALYPKII 240
QY 241 QDIETIESNMRCGRHSIORIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECK 300
DB 241 QDIETIESNMRCGRHSIORIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIMDKNTLECK 300
QY 301 RILTGHTGSLCLQYDERVYITGSSDSTVRVMDVTGEMLNTLIHCEAVLHLRFNNGM 360
DB 301 RILTGHTGSLCLQYDERVYITGSSDSTVRVMDVTGEMLNTLIHCEAVLHLRFNNGM 360
QY 361 VTCSKDRSIAVMDASPTDITLRLVVGHRAAVNVVDFDDKIYVSASGDRTIKVMNTSTC 420
DB 361 VTCSKDRSIAVMDASPTDITLRLVVGHRAAVNVVDFDDKIYVSASGDRTIKVMNTSTC 420
QY 421 EFVRTLNGHKGRIACIQYDRDLVVGSSDNTITLMDIEGACLRVLEGEHELVRCTIRFDN 480
DB 421 EFVRTLNGHKGRIACIQYDRDLVVGSSDNTITLMDIEGACLRVLEGEHELVRCTIRFDN 480

QY 481 KRIVGAYDGKIKVMDLVAALDPPAPAGTLCRLTVHSGRVFLQDFEFOIVSSSHDT 540
 DB 481 KRIVGAYDGKIKVMDLVAALDPPAPAGTLCRLTVHSGRVFLQDFEFOIVSSSHDT 540
 QY 541 ILIMDFLNDPAAQAEPSPSPRTTYTISR 569
 DB 541 ILIMDFLNDPAAQAEPSPSPRTTYTISR 569

RESULT 15
 AAY83254
 ID AAY83254 standard; protein; 569 AA.
 XX
 AC AAY83254;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE F-box protein FMD1p.
 XX
 KW Ubiquitin ligase; SCF; F-box protein; targeted degradation;
 KW destabilization; proteolysis; drug discovery; gene therapy; cancer;
 KW oncoprotein; Huntington's disease; gene knockout; delivery systems;
 KW mouse; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200022110-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-US023705.
 XX
 PR 09-OCT-1998; 98US-0103787P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Zhou P, Howley P;
 XX
 DR MPI, 2000-317970/27.
 DR N-PSDB; AA293714.
 XX
 PT Targeting degradation of polypeptide useful for treating cancer and other
 PT proliferative disorders, involves conjugating polypeptide with ubiquitin
 PT protein ligase or inhibiting ubiquitination using organic compound.
 XX
 PS Claim 9; Page 184-185; 185PP; English.
 XX
 CC The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin
 CC ligases) which can be used for the targeted degradation of a target
 CC polypeptide in vivo. Targeted degradation is achieved by expressing the
 CC ubiquitin ligase in a cell linked to the interaction domain of the target
 CC polypeptide and thereby recruiting the target polypeptide to the
 CC ubiquitin ligase. Such methods are useful for decreasing or increasing
 CC the level of a target polypeptide and for creating and expressing a
 CC destabilized polypeptide which is subjected to SCF mediated proteolysis.
 CC degrading any desired protein in a cell is useful for preventing or
 CC treating diseases caused by the presence of abnormal amount of the
 CC specific polypeptides, for drug discovery and for gene therapy. Diseases
 CC treated include cancer, by degradation of oncoproteins, Huntington's
 CC disease, other proliferative disorders and microbial infections. The
 CC method provides a quick and easy alternative to gene knockout technology.
 CC The target polypeptide can be degraded at all stages, or a specific
 CC stage, of development in the mature animal
 XX
 SQ Sequence 569 AA;

Query Match 98.8%; Score 2997; DB 3; Length 569;
 Best Local Similarity 98.6%; Pred. No. 3e-282;
 Matches 561; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDPAAVAVIQAELKFMNSSEKDCNNGEPKRIPEKNSLRQTYNSCARLCLNGETVCLIA 60
 DB 1 MDPAAVAVIQAELKFMNSSEKDCNNGEPKRIPEKNSLRQTYNSCARLCLNGETVCLIA 60

QY 61 STAKKTENCYAKTKLANGTSSMTIVPKORKLSASYEKEKEICVKKYFEQMSSESDOVEFEHL 120
 DB 61 STAKKTENCYAKTKLANGTSSMTIVPKORKLSASTEKEKEICVKKYFEQMSSESDOVEFEHL 120
 QY 121 ISQCHYQHGHINSYLRPMLQDFITLPAAGLDHIAENILSYLDAKSLCAELVCKEY 180
 DB 121 ISQCHYQHGHINSYLRPMLQDFITLPAAGLDHIAENILSYLDAKSLCAELVCKEY 180
 QY 181 RYISDGMIMKKLIERMVRTDSLWRGLAERGWGQYLFKNKPPDGNAPFNSFYRLAYEKII 240
 DB 181 RYISDGMIMKKLIERMVRTDSLWRGLAERGWGQYLFKNKPPDGNAPFNSFYRLAYEKII 240
 QY 241 QDIETISNNRCGRHSLORIHCRSETSKGYVCLQYDDOKIVSGLRDNTIKIMDQNTIECK 300
 DB 241 QDIETISNNRCGRHSLORIHCRSETSKGYVCLQYDDOKIVSGLRDNTIKIMDQNTIECK 300
 QY 241 QDIETISNNRCGRHSLORIHCRSETSKGYVCLQYDDOKIVSGLRDNTIKIMDQNTIECK 300
 DB 241 QDIETISNNRCGRHSLORIHCRSETSKGYVCLQYDDOKIVSGLRDNTIKIMDQNTIECK 300
 QY 301 RILGHTGSVLCQYDERVITITSSDSTVRVMDVNTGEMNTLIHCEAVLHLRFNNGM 360
 DB 301 RILGHTGSVLCQYDERVITITSSDSTVRVMDVNTGEMNTLIHCEAVLHLRFNNGM 360
 QY 361 VTGSKDRIAWMDASPTDITLRAVYVGHRAAVNVDPDDKTIYASAGDRTIKWNTSTC 420
 DB 361 VTGSKDRIAWMDASPTDITLRAVYVGHRAAVNVDPDDKTIYASAGDRTIKWNTSTC 420
 QY 421 EFVRTLNGHKGRIACLOYRDLVYSGSSDNTIRLMDIECGACULVLRGHEELVRCIFPDN 480
 DB 421 EFVRTLNGHKGRIACLOYRDLVYSGSSDNTIRLMDIECGACULVLRGHEELVRCIFPDN 480
 QY 481 KRIVGAYDGKIKVMDLVAALDPPAPAGTLCRLTVHSGRVFLQDFEFOIVSSSHDT 540
 DB 481 KRIVGAYDGKIKVMDLVAALDPPAPAGTLCRLTVHSGRVFLQDFEFOIVSSSHDT 540
 QY 541 ILIMDFLNDPAAQAEPSPSPRTTYTISR 569
 DB 541 ILIMDFLNDPAAQAEPSPSPRTTYTISR 569

Search completed: April 25, 2005, 16:34:17
 Job time : 174 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 16:06:41 / Search time 25 Seconds
(without alignments)
1699.013 Million cell updates/sec

Title: US-09-415-795-4

Perfect score: 3034

Sequence: 1 MDPAAVLAQEKALFKMNSSE.....PAAQAPPPSPRTYTIYSR 569

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3034	100.0	569	4	US-09-832-161-18 Sequence 18, Appl
2	3034	100.0	569	4	US-09-385-219A-2 Sequence 2, Appl
3	3034	100.0	569	4	US-09-601-168B-2 Sequence 2, Appl
4	2582.5	85.1	517	1	US-08-190-802A-30 Sequence 30, Appl
5	2582.5	85.1	517	3	US-08-477-346-30 Sequence 30, Appl
6	2582.5	85.1	517	3	US-08-473-089-30 Sequence 30, Appl
7	2582.5	85.1	517	3	US-08-487-072A-30 Sequence 30, Appl
8	2384.5	78.6	542	4	US-09-832-161-16 Sequence 16, Appl
9	644.5	21.2	626	4	US-09-213-888-21 Sequence 21, Appl
10	644.5	21.2	626	4	US-09-328-877D-21 Sequence 21, Appl
11	640	21.1	540	4	US-09-213-888-7 Sequence 7, Appl
12	640	21.1	540	4	US-09-213-888-10 Sequence 10, Appl
13	640	21.1	540	4	US-09-328-877D-7 Sequence 7, Appl
14	640	21.1	540	4	US-09-328-877D-10 Sequence 10, Appl
15	640	21.1	540	4	US-09-213-888-6 Sequence 6, Appl
16	640	21.1	545	4	US-09-328-877D-6 Sequence 6, Appl
17	640	21.1	553	4	US-09-213-888-5 Sequence 5, Appl
18	640	21.1	553	4	US-09-328-877D-5 Sequence 5, Appl
19	640	21.1	559	4	US-09-213-888-9 Sequence 9, Appl
20	640	21.1	559	4	US-09-328-877D-9 Sequence 9, Appl
21	640	21.1	589	4	US-09-213-888-8 Sequence 8, Appl
22	640	21.1	589	4	US-09-328-877D-8 Sequence 8, Appl
23	640	21.1	592	4	US-09-328-877D-4 Sequence 4, Appl
24	640	21.1	592	4	US-09-328-877D-4 Sequence 4, Appl
25	640	21.1	627	4	US-09-213-888-3 Sequence 3, Appl
26	640	21.1	627	4	US-09-328-877D-3 Sequence 3, Appl
27	640	21.1	666	4	US-09-213-888-27 Sequence 27, Appl

28	640	21.1	666	4	US-09-328-877D-27	Sequence 27, Appl
29	640	21.1	669	4	US-09-213-888-25	Sequence 25, Appl
30	640	21.1	669	4	US-09-328-877D-25	Sequence 25, Appl
31	545	18.0	640	4	US-09-177-165A-30	Sequence 30, Appl
32	520	17.1	587	3	US-08-899-578-2	Sequence 2, Appl
33	419.5	13.8	376	4	US-09-248-796A-14173	Sequence 14173, A
34	399	13.2	779	1	US-08-190-802A-32	Sequence 32, Appl
35	399	13.2	779	3	US-08-477-346-32	Sequence 32, Appl
36	399	13.2	779	3	US-08-473-089-32	Sequence 32, Appl
37	399	13.2	779	4	US-08-487-072A-32	Sequence 32, Appl
38	399	13.2	779	4	US-09-177-165A-29	Sequence 29, Appl
39	399	13.2	779	4	US-09-538-092-264	Sequence 264, App
40	392	12.9	732	3	US-08-914-999-8	Sequence 8, Appl
41	359.5	11.8	373	4	US-09-248-796A-18953	Sequence 18953, A
42	354	11.7	409	2	US-08-283-917-3	Sequence 3, Appl
43	354	11.7	409	2	US-08-961-716-3	Sequence 3, Appl
44	354	11.7	409	4	US-09-538-092-1119	Sequence 1119, Ap
45	354	11.7	410	2	US-08-283-917-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1					
US-09-832-161-18					
Sequence 18, Application US/09832161					
Patent No. 6656713					
GENERAL INFORMATION:					
APPLICANT: Manning, Anthony M.					
APPLICANT: Mercurio, Frank					
APPLICANT: Amle, Sharon					
APPLICANT: Ben-Neriah, Yimon					
APPLICANT: Davis, Matti					
APPLICANT: Hatzubai, Ada					
APPLICANT: Lavon, Iris					
APPLICANT: Yaron, Avraham					
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF					
FILE REFERENCE: NP-48					
CURRENT FILING DATE: 2001-04-09					
PRIOR APPLICATION NUMBER: 09/210,060					
PRIORITY FILING DATE: 1998-12-10					
NUMBER OF SEQ ID NOS: 30					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 18					
LENGTH: 569					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-09-832-161-18					
Query Match					
Best Local Similarity 100.0%; Score 3034; DB 4; Length 569;					
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	MDPAAVLAQEKALFKMNSSE	REDCNNGSPPKII	PEKSLAQTNYSCARL	CINQFTVCL 60
QY	61	STAKTEVCVAKTKLANGTSS	SMIVPQKRLTASYEKEKE	LCVKYEQMSQVFEVHL	120
DB	61	STAKTEVCVAKTKLANGTSS	SMIVPQKRLTASYEKEKE	LCVKYEQMSQVFEVHL	120
QY	121	ISOMCHYGHGINSYLAKEML	QRFDTALPARGLHIAENI	LSYDAKSLCAAEIVCKEWM	180
DB	121	ISOMCHYGHGINSYLAKEML	QRFDTALPARGLHIAENI	LSYDAKSLCAAEIVCKEWM	180
QY	181	RVTSDGMLMKTLIRRMVPT	SLMRGLAERBMGOYLFPNKR	PPDGAAPNSFYRALPYKII	240
DB	181	RVTSDGMLMKTLIRRMVPT	SLMRGLAERBMGOYLFPNKR	PPDGAAPNSFYRALPYKII	240
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Db 301 RILGHTGVSUCLQYDERVIIITGSSDSTVRWVDVNTGEMNTLIHCEAVLHLRPNNGM 360
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Db 361 VTCSKRSIAWDMASPTDITLRLVGHRAAVNVDPDDKXIYASAGDRTIKWNTSTC 420
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Db 481 KRIYSGAYDGKIKWMDVLAALDPPAPAGTLCRLTVHSGRVFRLQDFEQIVSSSHDT 540
Qy 541 ILIWFNDPAAQAEPSPSRITYTISR 569
Db 541 ILIWFNDPAAQAEPSPSRITYTISR 569

RESULT 2
US-09-385-219A-2
; Sequence 2, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chlaui, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-2

Query Match 100.0%; Score 3034; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 5.8e-314;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDPAAVLQEKALKFMNSEREDCNGEPKRIPEKNSLRQTYNSCARLCLNGETVCLA 60
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Db 61 STAKTENCVAKTLANGTSSMIVPKOKLSASYEKEKELCVKFEQWSESQVEFVHL 120
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Db 121 ISOMCHYOHGHINSYLKPMLOQDFITLAPAGLDHIAENILSYLDAKSLCAELVCKEMY 180
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Db 181 RVTSDGMLMKLIERMVRTDSLWRGLAERBGQYLFKNKPPDGNAPPNSFYRALYPKII 240
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Db 241 ODIEETESNWRGSRSLQRIHCRSETSKGVYCLQYDDQKIVSGLADNTIKIMDKNTLECK 300

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Db 541 ILIWFNDPAAQAEPSPSRITYTISR 569

RESULT 3
US-09-601-168B-2
; Sequence 2, Application US/09601168B
; Patent No. 6730486
; GENERAL INFORMATION:
; APPLICANT: BENAROUS, Richard
; APPLICANT: MARGOTTIN, Florence
; APPLICANT: DURAND, Hervé
; APPLICANT: ARENZANA SEISDEDOS, Fernando
; APPLICANT: KROLL, Mathias
; APPLICANT: CONDORCET, Jean-Paul
; TITLE OF INVENTION: Human beta-Ttcp protein
; FILE REFERENCE: 935.38812X00
; CURRENT APPLICATION NUMBER: US/09/601,168B
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: PCT/FR99/00196
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: FR98 01100
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR98 15545
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1 and manually
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence : cDNA
US-09-601-168B-2

Query Match 100.0%; Score 3034; DB 4; Length 569;
Best Local Similarity 100.0%; Pred. No. 5.8e-314;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDPAAVLQEKALKFMNSEREDCNGEPKRIPEKNSLRQTYNSCARLCLNGETVCLA 60
Db 1 MDPAAVLQEKALKFMNSEREDCNGEPKRIPEKNSLRQTYNSCARLCLNGETVCLA 60
Qy 61 STAKTENCVAKTLANGTSSMIVPKOKLSASYEKEKELCVKFEQWSESQVEFVHL 120
Db 61 STAKTENCVAKTLANGTSSMIVPKOKLSASYEKEKELCVKFEQWSESQVEFVHL 120
Qy 121 ISOMCHYOHGHINSYLKPMLOQDFITLAPAGLDHIAENILSYLDAKSLCAELVCKEMY 180
Db 121 ISOMCHYOHGHINSYLKPMLOQDFITLAPAGLDHIAENILSYLDAKSLCAELVCKEMY 180
Qy 181 RVTSDGMLMKLIERMVRTDSLWRGLAERBGQYLFKNKPPDGNAPPNSFYRALYPKII 240
Db 181 RVTSDGMLMKLIERMVRTDSLWRGLAERBGQYLFKNKPPDGNAPPNSFYRALYPKII 240

QY 241 ODIEETIESNMRCGRHSLOIRHCRSETSKGVYCLQYDDQKIYGLRDNTIKIMDKNTLECK 300
 DB 241 ODIEETIESNMRCGRHSLOIRHCRSETSKGVYCLQYDDQKIYGLRDNTIKIMDKNTLECK 300
 QY 301 RLITHTGTSVLCLOYDERVITIGSSDSIVRVWDVNTGEMLNTLIHHCBAVHLRFNNGMM 360
 DB 301 RLITHTGTSVLCLOYDERVITIGSSDSIVRVWDVNTGEMLNTLIHHCBAVHLRFNNGMM 360
 QY 361 VTCSDRSTIAVWDMASPDITILRVLVGRRVAVNVDPDDKXIYASGDRITIKWNTSTC 420
 DB 361 VTCSDRSTIAVWDMASPDITILRVLVGRRVAVNVDPDDKXIYASGDRITIKWNTSTC 420
 QY 421 BEVRLTNGHKGRIACLOYRDLVVSQSDNTIRLMDIEGACLRVLEGHBEIVRCIRPDN 480
 DB 421 BEVRLTNGHKGRIACLOYRDLVVSQSDNTIRLMDIEGACLRVLEGHBEIVRCIRPDN 480
 QY 481 KRIVGAYDGKIKWDLVAALDPAPAGTLCRTLVESGRVFRLOPDEFQIVSSSHDT 540
 DB 481 KRIVGAYDGKIKWDLVAALDPAPAGTLCRTLVESGRVFRLOPDEFQIVSSSHDT 540
 QY 541 ILIMFLNDPAAQAPRPSRSTTYISR 569
 DB 541 ILIMFLNDPAAQAPRPSRSTTYISR 569

RESULT 4

US-08-190-802A-30
 ; Sequence 30, Application US/08190802A
 ; Patent No. 5519003

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: P. O. Box 60850

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306-0850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/190,802A

FILING DATE: 01-FEB-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fabian, Gary R.

REGISTRATION NUMBER: 33,875

REFERENCE/DOCKET NUMBER: 8600-0139

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 517 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

ANTHETIC: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13

US-08-190-802A-30

Query Match 85.1%; Score 2582.5; DB 1; Length 517;

Best Local Similarity 91.4%; Pred. No. 6.5e-266;

Matches 487; Conservative 7; Mismatches 8; Indels 31; Gaps 2;

QY 18 SSEDNCNNGEPPRKIIPEKNSLRQTVNSCARLCLNGETVCLASTAMKTENCVAKTKLAN 77
 DB 13 ASEREDCNREDEPPRKIIPEKNTLRO-----TKLAN 42
 QY 78 GTSSMIVKORKLSAYEKELCVKYPEQWSESQVEVEHLISOMCHYGHINSYLK 137
 DB 43 GTSSMIVKORKLSAYEKELCVKYPEQWSESQVEVEHLISOMCHYGHINSYLK 102
 QY 138 PMLQDPFTTALPARGLDIAENIISYLDKSLCAAEVCKEMRYTSGMLMKKLIERNV 197
 DB 103 PMLQDPFTTALPARGLDIAENIISYLDKSLCAAEVCKEMRYTSGMLMKKLIERNV 162
 QY 198 RDTSLMRGLAARRGGVOLFKNKPPDGNA PPSFRAIYPKIIODIEETIESNMRCGRHSI 257
 DB 163 RDTSLMRGLAARRGGVOLFKNKPPDGNA PPSFRAIYPKIIODIEETIESNMRCGRHSI 222
 QY 258 QRHCRSETSKGVYCLQYDDQKIYGLRDNTIKIMDKNTLECKRLNGHTGTSVLCLOYDE 317
 DB 223 QRHCRSETSKGVYCLQYDDQKIYGLRDNTIKIMDKNTLECKRLNGHTGTSVLCLOYDE 282
 QY 318 RVITIGSSDSIVRVWDVNTGEMLNTLIHHCBAVHLRFNNGMMVTCSDRSTIAVWDMASP 377
 DB 283 RVITIG-SDSTIVRVWDVNTGEMLNTLIHHCBAVHLRFNNGMMVTCSDRSTIAVWDMASA 341
 QY 378 TDITLRRVLVGRRVAVNVDPDDKXIYASGDRITIKWNTSTCFEVRTLNGHKGRIACLO 437
 DB 342 TDITLRRVLVGRRVAVNVDPDDKXIYASGDRITIKWNTSTCFEVRTLNGHKGRIACLO 401
 QY 438 YRDLVVSQSDNTIRLMDIEGACLRVLEGHBEIVRCIRPDNKRIVGAYDGKIKWDL 497
 DB 402 YRDLVVSQSDNTIRLMDIEGACLRVLEGHBEIVRCIRPDNKRIVGAYDGKIKWDL 461
 QY 498 VAALDPAPAGTLCRTLVESGRVFRLOPDEFQIVSSSHDTIILMFLNDP 550
 DB 462 VAALDPAPAGTLCRTLVESGRVFRLOPDEFQIVSSSHDTIILMFLNDP 514

RESULT 5

US-08-477-346-30
 ; Sequence 30, Application US/08477346
 ; Patent No. 6262023

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: WD-40 - Derived Peptides and Uses

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Avenue, NW

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,346

FILING DATE: 07-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,072

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2550-0025.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

```

; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
; US-08-477-346-30

Query Match      85.1%; Score 2582.5; DB 3; Length 517;
Best Local Similarity 91.4%; Pred. No. 6.5e-266;
Matches 487; Conservative 7; Mismatches 8; Indels 31; Gaps 2;

QY 18 SSEREDCNNGEPKRIPEKNSLRQYNSCARLCLNQETVCLASTAMKTENCVAKTCLAN 77
DB 13 ASEREDCNRDEPPKRIITEKNTRLRQ-----TKLAN 42
QY 78 GTSSMIVKQKRLASYEKKEKLCVKYFEQWSESDQVEFVHLLISQCHYOHGHINSYLK 137
DB 43 GTSSMIVKQKRLASANYEKEKELCVKYFEQWSECDQVEFVHLLISRMCHYOHGHINTYLYK 102
QY 138 PMLORDFTTALPARGLDHIENILSYLDAKSLCAAEIVCKEWMYRVSQDMLMKKLIERNV 197
DB 103 PMLORDFTTALPARGLDHIENILSYLDAKSLCAAEIVCKEWMYRVSQDMLMKKLIERNV 162
QY 198 RTDSLMRGLAERRRGQYLFKNKPPDGNAPNSFYRALYPKLIQDIETISNMRCGRHSL 257
DB 163 RTDSLMRGLAERRRGQYLFKNKPPDGNAPNSFYRALYPKLIQDIETISNMRCGRHSL 222
QY 258 QRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLNGHTGSVLCLOYDE 317
DB 223 QRHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLNGHTGSVLCLOYDE 282
QY 318 RVIIITGSSDSTVRWVDNTGEMLNTLIHCEAVLHLRFNNGMWYTCSDKRSIAVDMAS 377
DB 283 RVIIITG-SDSTVRWVDNTGEMLNTLIHCEAVLHLRFNNGMWYTCSDKRSIAVDMASA 341
QY 378 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWNTSTCEFYVTLNGHKGIAQLQ 437
DB 342 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWNTSTCEFYVTLNGHKGIAQLQ 401
QY 438 YRDLRVVSGSSDNTIRLMDIEGACLRVLEGEHELVRCIRPDNKRIVSAGVDGKIKWDL 497
DB 402 YRDLRVVSGSSDNTIRLMDIEGACLRVLEGEHELVRCIRPDNKRIVSAGVDGKIKWDL 461
QY 498 VAALDPRAPAGTLCRLTVHSGRVFRLQDFEQIVSSSHDDTLLIWFPLNDP 550
DB 462 VAALDPRAPAGTLCRLTVHSGRVFRLQDFEQIVSSSHDDTLLIWFPLNDP 514

RESULT 6
US-08-473-089-30
; Sequence 30, Application US/08473089
; Patent No. 6342368
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESS: Morristown & Foerster
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,089
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 2550-0025.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 517 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
; US-08-473-089-30

Query Match      85.1%; Score 2582.5; DB 3; Length 517;
Best Local Similarity 91.4%; Pred. No. 6.5e-266;
Matches 487; Conservative 7; Mismatches 8; Indels 31; Gaps 2;

QY 18 SSEREDCNNGEPKRIPEKNSLRQYNSCARLCLNQETVCLASTAMKTENCVAKTCLAN 77
DB 13 ASEREDCNRDEPPKRIITEKNTRLRQ-----TKLAN 42
QY 78 GTSSMIVKQKRLASYEKKEKLCVKYFEQWSESDQVEFVHLLISQCHYOHGHINSYLK 137
DB 43 GTSSMIVKQKRLASANYEKEKELCVKYFEQWSECDQVEFVHLLISRMCHYOHGHINTYLYK 102
QY 318 RVIIITGSSDSTVRWVDNTGEMLNTLIHCEAVLHLRFNNGMWYTCSDKRSIAVDMAS 377
DB 283 RVIIITG-SDSTVRWVDNTGEMLNTLIHCEAVLHLRFNNGMWYTCSDKRSIAVDMASA 341
QY 378 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWNTSTCEFYVTLNGHKGIAQLQ 437
DB 342 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRITIKWNTSTCEFYVTLNGHKGIAQLQ 401
QY 438 YRDLRVVSGSSDNTIRLMDIEGACLRVLEGEHELVRCIRPDNKRIVSAGVDGKIKWDL 497
DB 402 YRDLRVVSGSSDNTIRLMDIEGACLRVLEGEHELVRCIRPDNKRIVSAGVDGKIKWDL 461
QY 498 VAALDPRAPAGTLCRLTVHSGRVFRLQDFEQIVSSSHDDTLLIWFPLNDP 550
DB 462 VAALDPRAPAGTLCRLTVHSGRVFRLQDFEQIVSSSHDDTLLIWFPLNDP 514

RESULT 7
US-08-487-072A-30
; Sequence 30, Application US/08487072A
; Patent No. 6423684
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
```


Db 452 DNKRIVSGAYDGKIKWMDLQALDPRAPASTLCLRTLVHSGRVFLQDFEQIISSHD 511
Qy 539 DTLLIWDLPNDPAQAEPSPSRRTTYISR 569
Db 512 DTLLIWDLPNDPAQAEPSPSRRTTYISR 542

RESULT 9
US-09-213-888-21

/ Sequence 21, Application US/09213888A
/ Patent No. 6638731
/ GENERAL INFORMATION:
/ APPLICANT: Gurney, Mark E.
/ APPLICANT: Li, Jinhe
/ APPLICANT: Pauley, Adele M.
/ APPLICANT: Pharmacia & Upjohn Company
/ TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
/ FILE REFERENCE: 6142
/ CURRENT APPLICATION NUMBER: US/09/213,888A
/ CURRENT FILING DATE: 1998-12-17
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 626
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
US-09-213-888-21

Query Match 21.2%; Score 644.5; DB 4; Length 626;
Best Local Similarity 30.1%; Pred. No. 3.1e-59;

Matches 169; Conservative 103; Mismatches 222; Indels 67; Gaps 15;

Qy 8 LQKALFKMNSEREDCNGEPKRIPEK--NSLRQ--TYNSCARLCLNOETVCLASTA 63
Db 53 MEQKLIBEDLNEMSLGDLTMEQKLIBEDLNEMSKRLDHGSEVRSFSLGKPKCKVSEY 112
Qy 64 MKNENCV-----AKTKLANGTSSMIVPKORKLSASYEKEL--CVKYFEQMSBD 112
Db 113 TSTTGLVPCSATPTTFEGDLRANOG-----QQRRTTSVQPPGLOEMLKMFGSMGPE 167
Qy 113 QVEFEHLISQWCHYGHGHSYLYKPMLODFITLPAAGLDHIAENILSYLDAKSLCAA 172
Db 168 KTLALDELIDSCERPTQVHMMQVIEPQRFDFISLP---KELALVYLSFLEPKDLLQA 223
Qy 173 ELVCKEWRVTSQGMIMKMLIERMVRTDSLMRGLAE---RRGMQYLFKNKPPDGNAP 227
Db 224 AOTCRVYRILAEADNLIMREKCKE-----EGIDELPHIKRRK-----VIKGFTHSP 269
Qy 228 PMSFYRALYPKIIODIETIESNMRGHRSLQRIHCRSETSKGVYCLQYDDQKIYGLRDN 287
Db 270 WKSAY-----IRQ--HRIDTMRGELKSPKV-LKGDHDIYITCLQFCGNRIYSGSDN 320
Qy 288 TIKIMDKNTLECKRILTGHTGVSVCLOYDERVLIITGSSDSTVRVMDVNTGEMTLIHHC 347
Db 321 TLKWSAVTGCRLTLVGHGTGVSWSQMRDNIISGSTDRILKVMNAETGECIHITLYGHT 380
Qy 348 EAVLHLRFNNGMVTCSDKRSIAVWDMASPTDITLRVLYVGHRAVNVVDPDDKIYVSAS 407
Db 381 STVRCMHLHERRVVSGRDATALRVMDIETGCL---HVLGMHVAAVRCVOYDGRVVSQA 437
Qy 408 GDRITKWNSTSCFEVRLTNGHKGIGIACLOYRDLVYSGSSDNTIRLMDIEGACLVYLE 467
Db 438 YDPMVKVMDPETETCCHITLQHTNRYVSLQPDGIHVVSGSLDTSIRVMDVETGNCIHITLT 497
Qy 468 GHEELVRCIRFNDKRIYSGAYDGKIKWMDLVAALDPRAPAGTLCLRTLV---EHSGRVFR 524
Db 498 GHQSILTSQEMELKDNILVSGNADSTYKIMDIKTG-----QCLQTLQGPNNKQSAVTC 548
Qy 525 LQDFEQIIVSSSHDDTLLIWD 545

Db 549 LQFNKNFVITSSDDGTIVKLMD 569

RESULT 10
US-09-328-877D-21

/ Sequence 21, Application US/09328877D
/ Patent No. 6730778
/ GENERAL INFORMATION:
/ APPLICANT: Gurney, Mark E.
/ APPLICANT: Li, Jinhe
/ APPLICANT: Pauley, Adele M.
/ APPLICANT: Pharmacia & Upjohn Company
/ TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
/ FILE REFERENCE: 6142
/ CURRENT APPLICATION NUMBER: US/09/328,877D
/ CURRENT FILING DATE: 1999-06-09
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 626
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
US-09-328-877D-21

Query Match 21.2%; Score 644.5; DB 4; Length 626;
Best Local Similarity 30.1%; Pred. No. 3.1e-59;
Matches 169; Conservative 103; Mismatches 222; Indels 67; Gaps 15;

Qy 8 LQKALFKMNSEREDCNGEPKRIPEK--NSLRQ--TYNSCARLCLNOETVCLASTA 63
Db 53 MEQKLIBEDLNEMSLGDLTMEQKLIBEDLNEMSKRLDHGSEVRSFSLGKPKCKVSEY 112
Qy 64 MKNENCV-----AKTKLANGTSSMIVPKORKLSASYEKEL--CVKYFEQMSBD 112
Db 113 TSTTGLVPCSATPTTFEGDLRANOG-----QQRRTTSVQPPGLOEMLKMFGSMGPE 167
Qy 113 QVEFEHLISQWCHYGHGHSYLYKPMLODFITLPAAGLDHIAENILSYLDAKSLCAA 172
Db 168 KTLALDELIDSCERPTQVHMMQVIEPQRFDFISLP---KELALVYLSFLEPKDLLQA 223
Qy 173 ELVCKEWRVTSQGMIMKMLIERMVRTDSLMRGLAE---RRGMQYLFKNKPPDGNAP 227
Db 224 AOTCRVYRILAEADNLIMREKCKE-----EGIDELPHIKRRK-----VIKGFTHSP 269
Qy 228 PMSFYRALYPKIIODIETIESNMRGHRSLQRIHCRSETSKGVYCLQYDDQKIYGLRDN 287
Db 270 WKSAY-----IRQ--HRIDTMRGELKSPKV-LKGDHDIYITCLQFCGNRIYSGSDN 320
Qy 288 TIKIMDKNTLECKRILTGHTGVSVCLOYDERVLIITGSSDSTVRVMDVNTGEMTLIHHC 347
Db 321 TLKWSAVTGCRLTLVGHGTGVSWSQMRDNIISGSTDRILKVMNAETGECIHITLYGHT 380
Qy 348 EAVLHLRFNNGMVTCSDKRSIAVWDMASPTDITLRVLYVGHRAVNVVDPDDKIYVSAS 407
Db 381 STVRCMHLHERRVVSGRDATALRVMDIETGCL---HVLGMHVAAVRCVOYDGRVVSQA 437
Qy 408 GDRITKWNSTSCFEVRLTNGHKGIGIACLOYRDLVYSGSSDNTIRLMDIEGACLVYLE 467
Db 438 YDPMVKVMDPETETCCHITLQHTNRYVSLQPDGIHVVSGSLDTSIRVMDVETGNCIHITLT 497
Qy 468 GHEELVRCIRFNDKRIYSGAYDGKIKWMDLVAALDPRAPAGTLCLRTLV---EHSGRVFR 524
Db 498 GHQSILTSQEMELKDNILVSGNADSTYKIMDIKTG-----QCLQTLQGPNNKQSAVTC 548
Qy 525 LQDFEQIIVSSSHDDTLLIWD 545
Db 549 LQFNKNFVITSSDDGTIVKLMD 569

```
RESULT 11
US-09-213-888-7
; Sequence 7, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 7
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-7

Query Match      21.1%; Score 640; DB 4; Length 540;
Best Local Similarity 30.8%; Pred. No. 7, 2e-59;
Matches 167; Conservative 92; Mismatches 211; Indels 72; Gaps 15;

QY      14 KFMSSEREDCNGSEPPKIIPEKNSLRQTYNSCARLCLNOBTVCIASTAMKTENCVAKT 73
DB      4 KLDHSEVRSFSLGKKPKV-----SEYSTTGL-----VPCSA-----TPTTFGLD 45
QY      74 KLANGTSMIYKQKRLSAYEKEKL--CYKFFQWSESDQVEVEHLISQMHYQCH 131
DB      46 RAANGQ-----QQRRTTSVOPPTGLQEWLMFQSWSGPEKLLADLIDSCPTQVGH 100
QY      132 INSYLKPMLODFITALPARGDHAENILSYLDKSLCAAEIVCKEWRVYVSDGMLWK 191
DB      101 MMQVIEPQGFQDFISLP---KELALYVLSFLEPKDLQAQOTCRYRIILAEIDLWRE 156
QY      192 LIERNVRTDSLWRGLAE-----RQWGQYLFKNKPPDGNAPNSFYRALYPKIIODIETI 246
DB      157 KCKE-----EGIDELHIKRRK-----VIKGFHSPWKSAY-----IRQ--HRI 194
QY      247 ESNMRCGHSIORIHCRSETSKGYVCLQYDDOKIYSGLRDNTIKWDKNTLECKRIILGH 306
DB      195 DTNMRGELKSPKV-LKGHDHVITCLOFCGNRIYSGSDNTLKYWSAVTGKCLRTLVGH 253
QY      307 TGSVLCLOYDERVITITSSDSTVRVWDVNTGEMLNTLHHCEAVLHLRPNNGMVTYCSKD 366
DB      254 TGGWSSQMRDNIISGSTDRTLKYMAETGECIHITLGHSTVACMLHKKRVVSGSRD 313
QY      367 RSIAYMDASPTDITLRLRVLVGHRAAVNVVDPDDKYIVASGDRITIKYWNSTCEFEVTL 426
DB      314 ATLRAWDIETGQCL---HVLGMHVAAYRCVQYDGRVYSGAYDFWVKWDPETETCLHTL 370
QY      427 NGHKGICLQYRDLVYSGSSDNTIRLMDIEGACLRVLEGHBLVRCIRPDNKRIVSG 486
DB      371 QGHTNRVYSLQFDGIHVYSGSLDTSIRWADVETGNCIHTLTGHOSLITSGMELKMDILVSG 430
QY      487 AYDGKIKYWDVAALDPAPAGTLCRLTV---EHSRGVFRLOPDEFOIVSSSHDITLI 543
DB      431 NADSTVKIWDITKG-----QCLQTLQGNPKQASAVTCLQFNKNFVITSSDDGTLYL 481
QY      544 WD 545
DB      482 WD 483

RESULT 12
US-09-213-888-10
; Sequence 10, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
```

```
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 10
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-213-888-10

Query Match      21.1%; Score 640; DB 4; Length 540;
Best Local Similarity 30.8%; Pred. No. 7, 2e-59;
Matches 167; Conservative 92; Mismatches 211; Indels 72; Gaps 15;

QY      14 KFMSSEREDCNGSEPPKIIPEKNSLRQTYNSCARLCLNOBTVCIASTAMKTENCVAKT 73
DB      4 KLDHSEVRSFSLGKKPKV-----SEYSTTGL-----VPCSA-----TPTTFGLD 45
QY      74 KLANGTSMIYKQKRLSAYEKEKL--CYKFFQWSESDQVEVEHLISQMHYQCH 131
DB      46 RAANGQ-----QQRRTTSVOPPTGLQEWLMFQSWSGPEKLLADLIDSCPTQVGH 100
QY      132 INSYLKPMLODFITALPARGDHAENILSYLDKSLCAAEIVCKEWRVYVSDGMLWK 191
DB      101 MMQVIEPQGFQDFISLP---KELALYVLSFLEPKDLQAQOTCRYRIILAEIDLWRE 156
QY      192 LIERNVRTDSLWRGLAE-----RQWGQYLFKNKPPDGNAPNSFYRALYPKIIODIETI 246
DB      157 KCKE-----EGIDELHIKRRK-----VIKGFHSPWKSAY-----IRQ--HRI 194
QY      247 ESNMRCGHSIORIHCRSETSKGYVCLQYDDOKIYSGLRDNTIKWDKNTLECKRIILGH 306
DB      195 DTNMRGELKSPKV-LKGHDHVITCLOFCGNRIYSGSDNTLKYWSAVTGKCLRTLVGH 253
QY      307 TGSVLCLOYDERVITITSSDSTVRVWDVNTGEMLNTLHHCEAVLHLRPNNGMVTYCSKD 366
DB      254 TGGWSSQMRDNIISGSTDRTLKYMAETGECIHITLGHSTVACMLHKKRVVSGSRD 313
QY      367 RSIAYMDASPTDITLRLRVLVGHRAAVNVVDPDDKYIVASGDRITIKYWNSTCEFEVTL 426
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US-09-328-877D-7
; Sequence 7, Application US/09328877D
; Patent No. 6730778
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
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RESULT 14
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: Sequence 10, Application US/09328877D
: Patent No. 6730778
: GENERAL INFORMATION:
: APPLICANT: Gurney, Mark E.
: APPLICANT: Li, Jinhe
: APPLICANT: Pauley, Adele M.
: APPLICANT: Pharmacia & Upjohn Company
: TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
: FILE REFERENCE: 6142
: FILE REFERENCE: Encode them
: CURRENT APPLICATION NUMBER: US/09/328,877D
: CURRENT FILING DATE: 1999-06-09
: NUMBER OF SEQ. ID NOS: 32
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 10

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RESULT 15
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; Sequence 6, Application US/09213888A
; Patent No. 6638731
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jinhe
; APPLICANT: Pauley, Adele M.
; APPLICANT: Pharmacia & Upjohn Company
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; TITLE OF INVENTION: Encode Them
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-213-888-6
Query Match      21.1%, Score 640, DB 4, Length 545;

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Best Local Similarity 30.8%; Pred. No. 7.4e-59;
Matches 167; Conservative 92; Mismatches 211; Indels 72; Gaps 15;

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QY 544 WD 545
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 25, 2005, 16:16:36 ; Search time 134 Seconds
(without alignments)
1413.120 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Published Applications AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3034	100.0	569	13 US-10-042-417-2	Sequence 2, Appli
3	3034	100.0	569	14 US-10-038-010-8	Sequence 8, Appli
4	3034	100.0	569	17 US-10-653-928-2	Sequence 2, Appli
5	2997	98.8	569	16 US-10-687-732-18	Sequence 18, Appli
6	2384.5	78.6	542	10 US-09-832-161-16	Sequence 16, Appli
7	2181	71.9	408	16 US-10-687-732-15	Sequence 15, Appli
8	1857.5	61.2	407	16 US-10-687-732-14	Sequence 14, Appli
9	1635.5	53.9	701	15 US-10-369-493-5420	Sequence 5420, Ap
10	1530	50.4	424	16 US-10-687-732-13	Sequence 13, Appli
11	1163	33.3	219	14 US-10-023-530-2	Sequence 2, Appli
12	989.5	32.6	265	9 US-09-764-848-30	Sequence 30, Appli
13	989.5	32.6	265	14 US-10-116-016-30	Sequence 30, Appli

14	989.5	32.6	265	14	US-10-222-020-30	Sequence 30, Appli
15	644.5	21.2	626	9	US-09-213-888-21	Sequence 21, Appli
16	644.5	21.2	626	9	US-09-328-877A-21	Sequence 21, Appli
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18	644.5	21.2	626	16	US-10-653-517-21	Sequence 21, Appli
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21	640	21.1	540	9	US-09-213-888-10	Sequence 10, Appli
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ALIGNMENTS

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US-09-832-161-18
; Sequence 18, Application US/09832161
; Publication No. US20030166587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yinon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Itis
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF-KB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-161-18

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Best Local Similarity 100.0%; Pred. No. 8.5e-270;
Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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; Publication No. US20020123082A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/10/042,417
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-417-2
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Best Local Similarity 100.0%; Pred. No. 8.5e-270;
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; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS
; APPLICANT: Pierre, Legrain
; TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
; FILE REFERENCE: B4767A
; CURRENT APPLICATION NUMBER: US/10/038,010
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US 60/259,377
; PRIOR FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: beta-T-CPI
; LOCATION: (1)..(569)
; OTHER INFORMATION:
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Matches 569; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-10-652-928-2
; Sequence 2, Application US/10652928
; Publication No. US20050079558A1
; GENERAL INFORMATION:
; APPLICANT: Chaur, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/652,928
; CURRENT FILING DATE: 2003-08-28
; PRIOR APPLICATION NUMBER: US/09/385,219A
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-652-928-2

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Db 61 STAMKTENCVAATKLANGTSSMIIVKORLKSASYEKEKELCVKYFEQWSESQDFEVEHL 120
Qy 121 ISOMCHYOHGHINSYILKPMLOPDTLALPARGLDHAENIISYLDKSLCAAEIVCKEY 180
Db 121 ISOMCHYOHGHINSYILKPMLOPDTLALPARGLDHAENIISYLDKSLCAAEIVCKEY 180
Qy 181 RVTSDGMLWKLIERNVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
Db 181 RVTSDGMLWKLIERNVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240

Db 181 RVTSDGMLWKLIERNVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
Qy 241 ODLETESNMRGRSLORIHCRSETSKGVYCLQYDDOKIYVGLRNTIKIMDKNTLECK 300
Db 241 ODLETESNMRGRSLORIHCRSETSKGVYCLQYDDOKIYVGLRNTIKIMDKNTLECK 300
Qy 301 RLITGHTGSLVLCQYDERVIITGSSDSYRVWMDVNTGEMLNTLIHHCBAVLHLRFNNGM 360
Db 301 RLITGHTGSLVLCQYDERVIITGSSDSYRVWMDVNTGEMLNTLIHHCBAVLHLRFNNGM 360
Qy 361 VTCSKORSIAVWDMASPTDITLRRVLVGHRAAVNVDPDDKIYVSGDRITIKWNTSTC 420
Db 361 VTCSKORSIAVWDMASPTDITLRRVLVGHRAAVNVDPDDKIYVSGDRITIKWNTSTC 420
Qy 421 EFVRTLNHKGRIACIQYRDLRVVSGSSDNTIRLWDIEGACLRVLEHGEELVRCIRFND 480
Db 421 EFVRTLNHKGRIACIQYRDLRVVSGSSDNTIRLWDIEGACLRVLEHGEELVRCIRFND 480
Qy 481 KRIVGAYDGKIKWMDLVAAIDPRAPAGTLCRTLVHSGRVRLQDFEQIVSSSHDT 540
Db 481 KRIVGAYDGKIKWMDLVAAIDPRAPAGTLCRTLVHSGRVRLQDFEQIVSSSHDT 540
Qy 541 ILIWFNDPAAQAEPPSPSRRTYIYISR 569
Db 541 ILIWFNDPAAQAEPPSPSRRTYIYISR 569

RESULT 5

US-10-687-732-18
; Sequence 18, Application US/10687732
; Publication No. US20040171074A1
; GENERAL INFORMATION:
; APPLICANT: Olicky, Stephen
; APPLICANT: Sichert, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; APPLICANT: Tang, Xiaodong
; TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
; FILE REFERENCE: 14096.34USU1
; CURRENT APPLICATION NUMBER: US/10/687,732
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,606
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 18
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank/NP_033901
; DATABASE ENTRY DATE: 1998-08-04
; RELEVANT RESIDUES: (1)..(569)
US-10-687-732-18

Query Match 98.8%; Score 2897; DB 16; Length 569;
Best Local Similarity 98.6%; Pred. No. 2.1e-266;
Matches 561; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MDPAAVLOEAKLKPMNSEREDCNGBPRIIPEKNSLRQYNSCARLCINQETVCL 60
Db 1 MDPAAVLOEAKLKPMNSEREDCNGBPRIIPEKNSLRQYNSCARLCINQETVCL 60
Qy 61 STAMKTENCVAATKLANGTSSMIIVKORLKSASYEKEKELCVKYFEQWSESQDFEVEHL 120
Db 61 STAMKTENCVAATKLANGTSSMIIVKORLKSASYEKEKELCVKYFEQWSESQDFEVEHL 120
Qy 121 ISOMCHYOHGHINSYILKPMLOPDTLALPARGLDHAENIISYLDKSLCAAEIVCKEY 180
Db 121 ISOMCHYOHGHINSYILKPMLOPDTLALPARGLDHAENIISYLDKSLCAAEIVCKEY 180
Qy 181 RVTSDGMLWKLIERNVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
Db 181 RVTSDGMLWKLIERNVRTDSLWRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240

Db 181 RVTSQDMLMKLIERHVRVTDLSLWGLAERBGWGYLFKNKRPDENAPNSFYRALYPKII 240
Qy 241 ODIEETIESNMWRCGRSLORIHCRSETSKGVYCLQYDDOKIYSGADNNTIKIMDKNTLECK 300
Db 241 ODIEETIESNMWRCGRSLORIHCRSETSKGVYCLQYDDOKIYSGADNNTIKIMDKNTLECK 300
Qy 301 RLITGHTGSVLCLQYDERVIITIGSSDSSTYRVWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360
Db 301 RLITGHTGSVLCLQYDERVIITIGSSDSSTYRVWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360
Qy 361 VTCSKORSIAVWDMASPTDITLRRVYVGHRAAVNVVDFDDKXIYASGDRITIKWNTSTC 420
Db 361 VTCSKORSIAVWDMASPTDITLRRVYVGHRAAVNVVDFDDKXIYASGDRITIKWNTSTC 420
Qy 421 BEVRLTNGHKRGIACTQYRDRLVWSSGSDNNTIRLMDIEGACTRLVLEGHEELVRCIRF 480
Db 421 BEVRLTNGHKRGIACTQYRDRLVWSSGSDNNTIRLMDIEGACTRLVLEGHEELVRCIRF 480
Qy 481 KRIVGAYDGKIKWDLVAALDPRAPAGTLCRTLVHSGRVFLQDFEQIVSSSHDT 540
Db 481 KRIVGAYDGKIKWDLVAALDPRAPAGTLCRTLVHSGRVFLQDFEQIVSSSHDT 540
Qy 541 ILIWDPLNDPAAQAEPSPSRRTTYISR 569
Db 541 ILIWDPLNDPAAQAEPSPSRRTTYISR 569

RESULT 6

US-09-832-161-16
; Sequence 16, Application US/09832161
; Publication No. US2003016587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
; APPLICANT: Mercurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Ben-Neriah, Yimon
; APPLICANT: Davis, Matti
; APPLICANT: Hatzubai, Ada
; APPLICANT: Lavon, Iris
; APPLICANT: Yaron, Avraham
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
; TITLE OF INVENTION: NF-kB
; FILE REFERENCE: 860098.427
; CURRENT APPLICATION NUMBER: US/09/832,161
; PRIOR FILING DATE: 2001-04-09
; CURRENT APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-161-16

Query Match 78.6%; Score 2384.5; DB 10; Length 542;
Best Local Similarity 79.0%; Pred. No. 4.2e-210;
Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;

Qy 1 MDPAAVLQKALFKPNSREDNNNGEPKRIIPEKNSLRQTYNSCARLCLINQETVCLA 60
Db 1 MDPAAVLQKALFKPNSREDNNNGEPKRIIPEKNSLRQTYNSCARLCLINQETVCLA 60
Qy 61 S--TAMKTNCVAKTKYLANGTSMIVPKORUKLSAYEKEKELCVKFFQWSSDQVEFE 118
Db 61 S--TAMKTNCVAKTKYLANGTSMIVPKORUKLSAYEKEKELCVKFFQWSSDQVEFE 118
Qy 37 SCLQSPVYVCL--QISNGTSSVIVSRKPSBEGNVQKEDLCIKYFDQWSESDDVEFE 93
Db 37 SCLQSPVYVCL--QISNGTSSVIVSRKPSBEGNVQKEDLCIKYFDQWSESDDVEFE 93
Qy 119 HLISQCHYQHGHINSYLPMLQRPDITLPAKGLDHTAENTLSYLDASLCAALYCKE 178
Db 119 HLISQCHYQHGHINSYLPMLQRPDITLPAKGLDHTAENTLSYLDASLCAALYCKE 178
Qy 94 HLISQCHYQHGHINSYLPMLQRPDITLPAKGLDHTAENTLSYLDASLCAALYCKE 153
Db 94 HLISQCHYQHGHINSYLPMLQRPDITLPAKGLDHTAENTLSYLDASLCAALYCKE 153
Qy 179 WYRVTSQDMLMKLIERHVRVTDLSLWGLAERBGWGYLFKNKRPDGNAPNSFYRALYPK 238
Db 179 WYRVTSQDMLMKLIERHVRVTDLSLWGLAERBGWGYLFKNKRPDGNAPNSFYRALYPK 238

Db 154 WQVITSEGMMLMKLIERHVRVTDPLMKGLSRRGWGYLFKNRPDTG--PNSFYRSLYPK 211
Qy 239 IIODIEETIESNMWRCGRSLORIHCRSETSKGVYCLQYDDOKIYSGADNNTIKIMDKNTLE 298
Db 212 IIODIEETIESNMWRCGRSLORIHCRSETSKGVYCLQYDDOKIYSGADNNTIKIMDKNTLE 271
Qy 299 CKRLITGHTGSVLCLQYDERVIITIGSSDSSTYRVWVDVNTGEMLNTLIHCEAVLHLRFNNGM 358
Db 272 CKRLITGHTGSVLCLQYDERVIITIGSSDSSTYRVWVDVNTGEMLNTLIHCEAVLHLRFNNGM 331
Qy 359 MMTVCSKORSIAVWDMASPTDITLRRVYVGHRAAVNVVDFDDKXIYASGDRITIKWNTS 418
Db 332 LMVCSKORSIAVWDMASPTDITLRRVYVGHRAAVNVVDFDDKXIYASGDRITIKWNTS 391
Qy 419 TCEVRLTNGHKRGIACTQYRDRLVWSSGSDNNTIRLMDIEGACTRLVLEGHEELVRCIRF 478
Db 392 TCEVRLTNGHKRGIACTQYRDRLVWSSGSDNNTIRLMDIEGACTRLVLEGHEELVRCIRF 451
Qy 479 DNKRIVGAYDGKIKWDLVAALDPRAPAGTLCRTLVHSGRVFLQDFEQIVSSSHD 538
Db 452 DNKRIVGAYDGKIKWDLVAALDPRAPAGTLCRTLVHSGRVFLQDFEQIVSSSHD 511
Qy 539 DTIIWDPLNDPAAQAEPSPSRRTTYISR 569
Db 512 DTIIWDPLNDPAAQAEPSPSRRTTYISR 542

RESULT 7

US-10-687-732-15
; Sequence 15, Application US/10687732
; Publication No. US2004017107A1
; GENERAL INFORMATION:
; APPLICANT: Orlicky, Stephen
; APPLICANT: Siebert, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Williams, Andrew
; APPLICANT: Tang, Xiaojing
; TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
; FILE REFERENCE: 14096.34USU1
; CURRENT APPLICATION NUMBER: US/10/687,732
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,606
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-687-732-15

Query Match 71.9%; Score 2181; DB 16; Length 408;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 140 LQRPDITLPAKGLDHTAENTLSYLDASLCAALYCKEYRVTSQDMLMKLIERHVR 199
Db 1 LQRPDITLPAKGLDHTAENTLSYLDASLCAALYCKEYRVTSQDMLMKLIERHVR 199
Qy 200 DSLWGLAERBGWGYLFKNKRPDGNAPNSFYRALYPKIIODIEETIESNMWRCGRSLOR 259
Db 200 DSLWGLAERBGWGYLFKNKRPDGNAPNSFYRALYPKIIODIEETIESNMWRCGRSLOR 259
Qy 61 DSLWGLAERBGWGYLFKNKRPDGNAPNSFYRALYPKIIODIEETIESNMWRCGRSLOR 120
Db 61 DSLWGLAERBGWGYLFKNKRPDGNAPNSFYRALYPKIIODIEETIESNMWRCGRSLOR 120
Qy 260 IHCRSETSKGVYCLQYDDOKIYSGADNNTIKIMDKNTLECKRLITGHTGSVLCLQYDERV 319
Db 121 IHCRSETSKGVYCLQYDDOKIYSGADNNTIKIMDKNTLECKRLITGHTGSVLCLQYDERV 180
Qy 320 IITSSDSSTYRVWVDVNTGEMLNTLIHCEAVLHLRFNNGMVTSKORSIAVWDMASPTD 379
Db 181 IITSSDSSTYRVWVDVNTGEMLNTLIHCEAVLHLRFNNGMVTSKORSIAVWDMASPTD 240
Qy 380 IITLRRVYVGHRAAVNVVDFDDKXIYASGDRITIKWNTSTCEVRLTNGHKRGIACTQYR 439
Db 380 IITLRRVYVGHRAAVNVVDFDDKXIYASGDRITIKWNTSTCEVRLTNGHKRGIACTQYR 439

Db 241 ILLRVLVGHRAAVNVVDDDKYIVSASGDRITIKWNTSTCEFRVTLNGHKGIAQLQYR 300
QY 440 DDLVYSGSSDNTIRLMDIEGACLRLEGEHELVRCIRPDNKRIVSAGADGKIYWDLVA 499
Db 301 DDLVYSGSSDNTIRLMDIEGACLRLEGEHELVRCIRPDNKRIVSAGADGKIYWDLVA 360
QY 500 ALDPPAAGTLCRLTVESHSGRVFLQDFEQIVSSSHDITLIIMDFL 547
Db 361 ALDPPAAGTLCRLTVESHSGRVFLQDFEQIVSSSHDITLIIMDFL 408

RESULT 8

US-10-687-732-14
; Sequence 14, Application US/10687732
; Publication No. US20040171074A1
; GENERAL INFORMATION:
; APPLICANT: Orlicky, Stephen
; APPLICANT: Sicheil, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew
; APPLICANT: Tang, Xiaojing
; TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
; FILE REFERENCE: 14096.34US01
; CURRENT APPLICATION NUMBER: US/10/687,732
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/419,606
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-687-732-14

Query Match 61.2%; Score 1857.5; DB 16; Length 407;
Best Local Similarity 85.0%; Pred. No. 8.1e-162;
Matches 347; Conservative 30; Mismatches 30; Indels 1; Gaps 1;

QY 140 LORDITLTPARGLDHIAENILSYLDAKSLCAELVCEKWRYVSDGMLMKLIERMVT 199
Db 1 LORDITLTPARGLDHIAENILSYLDAKSLCAELVCEKWRYVSDGMLMKLIERMVT 60
QY 200 DDLVYSGSSDNTIRLMDIEGACLRLEGEHELVRCIRPDNKRIVSAGADGKIYWDLVA 259
Db 61 DDLVYSGSSDNTIRLMDIEGACLRLEGEHELVRCIRPDNKRIVSAGADGKIYWDLVA 119
QY 260 IHCRESYSGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRILNGHTGSVCLQYDERV 319
Db 120 IHCRESYSGVYCLQYDDQKIVSGLRDNTIKIMDKNTLECKRILNGHTGSVCLQYDERV 179
QY 320 IITGSSDSSTVRVWVDVNTGEMTLIHCEAVLHLRPNNGMVTCSKDRSIAVMDASPTD 379
Db 180 IITGSSDSSTVRVWVDVNTGEMTLIHCEAVLHLRPNNGMVTCSKDRSIAVMDASPTD 239
QY 380 ILLRVLVGHRAAVNVVDDDKYIVSASGDRITIKWNTSTCEFRVTLNGHKGIAQLQYR 439
Db 240 ILLRVLVGHRAAVNVVDDDKYIVSASGDRITIKWNTSTCEFRVTLNGHKGIAQLQYR 299
QY 440 DDLVYSGSSDNTIRLMDIEGACLRLEGEHELVRCIRPDNKRIVSAGADGKIYWDLVA 499
Db 300 DDLVYSGSSDNTIRLMDIEGACLRLEGEHELVRCIRPDNKRIVSAGADGKIYWDLVA 359
QY 500 ALDPPAAGTLCRLTVESHSGRVFLQDFEQIVSSSHDITLIIMDFL 547
Db 360 ALDPPAAGTLCRLTVESHSGRVFLQDFEQIVSSSHDITLIIMDFL 407

RESULT 9
US-10-369-493-5420
; Sequence 5420, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5420
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5420

Query Match 53.9%; Score 1635.5; DB 15; Length 701;
Best Local Similarity 57.7%; Pred. No. 4.6e-141;
Matches 328; Conservative 69; Mismatches 116; Indels 55; Gaps 8;

QY 31 RKIPEKSLRQTVNSCARLCUNQETVCLASTAMKTENCVAKTLAN-----GTS 80
Db 2 RRFREGKALKRGARADGSGIQLATVCST-----IERCF--TAVSNPIFLPSTFFSVF 55
QY 81 SMIVPKQR-----KLASYEKEKELCVKYPFGQSSSDQVEVHLISQCHYQHGHINSY 135
Db 56 SFLPSPRMTQIFLVSRSFSFSFSEVL-----KMSHEQLDFMDKIVHRLSHYQLGVDF 110
QY 136 LKPMLOPDTLTPARGLDHIAENILSYLDAKSLCAELVCEKWRYVSDGMLMKLIER 195
Db 111 IRPMLQRPISMLP-----HLVELILFVNVSLSLCSBSTSWCALARGQHWKLIK 166
QY 236 YPKIIDIETTESNRCGRHSIQRHCRSEYSGVYCLQYDDQKIVSGLRDNTIKIMDKN 295
Db 227 YPKIIRIDHINIDNMKRGVYKWTIRNCSSENSKGYCLQYDDQKIVSGLRDNTIKIMDKN 286
QY 236 TLECKRIITLGHVSTLCLQYDERVITGSSDSSTVRVWVDVNTGEMTLIHCEAVLHLR 355
Db 287 DYCSRIISGHTGSLCLQYDNRVILSSSDATVWVVEGECIKTLIHCEAVLHLR 346
QY 356 NNGMNVTSKDRSIAVMDASPTDITLRRVLVGHRAAVNVVDDDKYIVSAGDRTIKW 415
Db 347 ANGINVTSKDRSIAVMDASPTDITLRRVLVGHRAAVNVVDDDKYIVSAGDRTIKW 406
QY 416 NTSTCEFRVTLNGHKGIAQLQYDRLVYSGSSDNTIRLMDIEGACLRLEGEHELVRC 475
Db 407 SMDTLFVRTLHGRHGIACLQYRGLVYSGSSDNTIRLMDIEGACLRLEGEHELVRC 466
QY 476 IRFDNKRIVSAGADGKIYWDLVAALDPPAAGTLCRLTVESHSGRVFLQDFEQIVSS 535
Db 467 IRFDNKRIVSAGADGKIYWDLVAALDPPAAGTLCRLTVESHSGRVFLQDFEQIVSS 526
QY 536 SHDDITLIIMDFLNDPAAQAEPPRSPRT 563
Db 527 SHDDITLIIMDFLNDPAAQAEPPRSPRT 549

RESULT 10
US-10-687-732-13
; Sequence 13, Application US/10687732
; Publication No. US20040171074A1
; GENERAL INFORMATION:
; APPLICANT: Orlicky, Stephen
; APPLICANT: Sicheil, Frank
; APPLICANT: Tyers, Mike
; APPLICANT: Willems, Andrew

APPLICANT: Tang, Xiaojing
TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCR Complexes
FILE REFERENCE: 14096.34USU1
CURRENT APPLICATION NUMBER: US/10/667,732
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: US 60/419,606
PRIOR FILING DATE: 2002-10-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.2
SEQ ID NO 13
LENGTH: 424
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-10-667-732-13

Query Match 50.4%; Score 1530; DB 16; Length 424;
Best Local Similarity 69.2%; Pred. No. 1,1e-133;
Matches 296; Conservative 38; Mismatches 70; Indels 24; Gaps 2;

QY 140 LORDITLPAAGLDHIAENITLSDAKSLCAELVCKEYRVTSDDGLMKKLIERMRT 199
DB 1 LORDITSLNLP---HLVELLFNVNSDSLKSCSEVSTSWRCALARGQHKKLIKKNVRS 56
QY 200 DSLMGLAERGMGQYL-----FKNKPPDGNAPPNSEFYRALYFKI 239
DB 57 DSLMGLSEKRWKMDKFLNISRDMSVRI CEKFNVDVNI KDKLDQLIMHVFYSKLYPKI 116
QY 240 IODITTESNRCGHSIORHCRSETSKGYCLOYDQKIYSGIRDNTIKIWDKNTIEC 299
DB 117 IRDINHNNMWRGKGYKMTIRINCOSENSGYCLOYDDKIKVSGIRDNTIKIWDKNSC 176
QY 300 KRILLGHTGSVLCLOYDERVITTSDDSTVRVMDVNTGEMLNTLHHCEAVLHLPNNGM 359
DB 177 SRLSGHTGSVLCLOYDNRVITSSGSDATVRVMDVETGCTKLTLHCEAVLHLPFANGI 236
QY 360 MWTGSKDSIAVMDASPTDITLRVVLVGHRAAVNVVFDDEKYIVSASGDRITIKYMTST 419
DB 237 MWTGSKDSIAVMDVSPDITIRVVLVGHRAAVNVVFDDEKYIVSASGDRITIKYMSMT 296
QY 420 CEFVTLNGHKRGIACTQYRDLVVGSSDNTIRIMDJECAGCLVYLSGHEELVRCIRPD 479
DB 297 LEFVTLNGHRRGIACTQYRGLVVGSSDNTIRIMDJHSGCLVYLSGHEELVRCIRPD 356
QY 480 NKRIYSGAVDGIKIVMDLVAALDPRAPAGTLCRLTVSHSGVRFLOPDEFOIVSSHDD 539
DB 357 EKRIYSGAVDGIKIVMDLVAALDPRALSEITCLSLVQHTGKRVFRLQFPDFIVSSSHD 416
QY 540 TILIMDFL 547
DB 417 TILIMDFL 424

RESULT 11
US-10-023-530-2
Sequence 2, Application US/10023530
Publication No. US20030007956A1
GENERAL INFORMATION:
APPLICANT: LEGRAIN, Pierre
APPLICANT: BENAROUS, Richard
APPLICANT: BLOT, Guillaume
APPLICANT: LASSOT, Irina
TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TROP
FILE REFERENCE: B4717A
CURRENT APPLICATION NUMBER: US/10/023,530
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: 60/256,276
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: BetaTrop
LOCATION: (1)..(219)
OTHER INFORMATION: F-box protein
US-10-023-530-2

Query Match 38.3%; Score 1163; DB 14; Length 219;
Best Local Similarity 100.0%; Pred. No. 2.4e-98;
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALFKMNSEREDCNNGEPPRKIIPEKNSLRQYNSCARLCLNQETVCLA 60
DB 1 MDPAAVLQEKALFKMNSEREDCNNGEPPRKIIPEKNSLRQYNSCARLCLNQETVCLA 60
QY 61 STAKTENCVAKTLANGTSMIVPKRKLSASYEKEKELCVKFEQMSSEDOVEFVHL 120
DB 61 STAKTENCVAKTLANGTSMIVPKRKLSASYEKEKELCVKFEQMSSEDOVEFVHL 120
QY 121 ISOMCHYOHGHINSYLPMLORDFTLPAAGLDHIAENITLSDAKSLCAELVCKEY 180
DB 121 ISOMCHYOHGHINSYLPMLORDFTLPAAGLDHIAENITLSDAKSLCAELVCKEY 180
QY 181 RVTSDGMLMKKLIERMVRTDSLWGLAERGMGQYLFKN 219
DB 181 RVTSDGMLMKKLIERMVRTDSLWGLAERGMGQYLFKN 219

RESULT 12
US-09-764-848-30
Sequence 30, Application US/09764848
Patent No. US20020077270A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT208
CURRENT APPLICATION NUMBER: US/09/764,848
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 265
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-848-30

Query Match 32.6%; Score 989.5; DB 9; Length 265;
Best Local Similarity 68.9%; Pred. No. 2.9e-82;
Matches 186; Conservative 24; Mismatches 21; Indels 39; Gaps 3;

QY 15 FMNSEREDCNNGEPPRKIIPEKNSLRQYNSCARLCLNQETVCLASTAKTENCVAKT 74
DB 20 FMNSEREDCNNGEPPRKIIPEKNSLRQYNSCARLCLNQETVCLASTAKTENCVAKT 74
QY 75 LANGTSMIVPKRKLSASYEKEKELCVKFEQMSSEDOVEFVHLISOMCHYOHGHINS 134
DB 43 ISNGTSSIVYRKRPSEGNVYKEKDLCTKYTDQSESDQVBFVHLSRMCHYOHGHINS 102
QY 135 YLKPMLODFITLPAAGLDHIAENITLSDAKSLCAELVCKEYRVTSDDGLMKKLI 194
DB 103 YLKPMLODFITLPAAGLDHIAENITLSDAKSLCAELVCKEYRVTSDDGLMKKLI 162
QY 195 RMVNTDSLWGLAERGMGQYLFKNKPPDGNAPPNSEFYRALYFKI IODITTESNRCGR 254
DB 163 RMVNTDSLWGLAERGMGQYLFKNKPPDGNAPPNSEFYRALYFKI IODITTESNRCGR 220
QY 255 HSLORIHCRSETSKGYCLOYDQKIYSG 284
DB 221 HSLORIHCRSETSKGYCLOYDQKIYSG 250

RESULT 13
US-10-116-016-30

```
/ Sequence 30, Application US/10116016
/ Publication No. US20030054379A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT208C1
/ CURRENT APPLICATION NUMBER: US/10/116,016
/ CURRENT FILING DATE: 2002-04-05
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 30
/ LENGTH: 265
/ TYPE: prt
/ ORGANISM: Homo sapiens
US-10-116-016-30

Query Match      32.6%; Score 989.5; DB 14; Length 265;
Best Local Similarity 68.9%; Pred. No. 2,9e-82;
Matches 186; Conservative 24; Mismatches 21; Indels 39; Gaps 3;

QY 15 FMNSEREDCNNGEPPRKTIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAATK 74
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 20 FQNTSVMEQDESPK-----KNTLMQ-----42

QY 75 LANGSSMTVPRKQKRLASYEKEKELCVKYEFEOMSESDOVEFEHLISQMCHYGHINS 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 43 ISNGSVSVSVSRKRSEGVYQKEKDLCKYFQWSESDVEFEHLISMCYHGHINS 102

QY 135 YKPEMLQDFITALPARGDHAENILSYLDAKSLCAELVCKEWRYVTSQMLMKKLE 194
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 103 YKPEMLQDFITALPARGDHAENILSYLDAKSLCAELVCKEWRYVTSQMLMKKLE 162

QY 195 RMVRTDSLRLGLAERGGQYLFKPKPDGNAPEPNSFYALYPKTIIDITETESWRCR 254
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 163 RMVRTDPLMKGLSERGGQYLFKPKPTDG--PEPNSFYALYPKTIIDITETESWRCR 220

QY 255 HSLRHCRESKSGVYCCQYVDOKIVSGL 284
Db 221 HMLQRIQCRSENSKGYVCLQYDDEKISGL 250

RESULT 14
US-10-222-020-30
/ Sequence 30, Application US/10222020
/ Publication No. US20030175739A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT208C2
/ CURRENT APPLICATION NUMBER: US/10/222,020
/ CURRENT FILING DATE: 2002-08-16
/ PRIOR APPLICATION NUMBER: 10/116,016
/ PRIOR FILING DATE: 2002-04-05
/ PRIOR APPLICATION NUMBER: 09/764,848
/ PRIOR FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: 60/179,065
/ PRIOR FILING DATE: 2000-01-31
/ PRIOR APPLICATION NUMBER: 60/180,628
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: 60/214,886
/ PRIOR FILING DATE: 2000-06-28
/ PRIOR APPLICATION NUMBER: 60/217,487
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/ PRIOR APPLICATION NUMBER: 60/225,758
/ PRIOR FILING DATE: 2000-08-14
/ PRIOR APPLICATION NUMBER: 60/220,963
/ PRIOR FILING DATE: 2000-07-26
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/ PRIOR APPLICATION NUMBER: 60/225,447
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/ PRIOR APPLICATION NUMBER: 60/216,647
/ PRIOR FILING DATE: 2000-07-07
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/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: 60/241,785
/ PRIOR FILING DATE: 2000-10-20
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/ PRIOR APPLICATION NUMBER: 60/236,370
/ PRIOR FILING DATE: 2000-09-29
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;; PRIOR FILING DATE: 2000-10-02
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;; PRIOR APPLICATION NUMBER: 60/246,475
;; PRIOR FILING DATE: 2000-11-08

Query Match 32.6%; Score 989.5; DB 14; Length 265;

Best Local Similarity 66.9%; Pred. No. 2.9e-82; Matches 186; Conservative 24; Mismatches 21; Indels 39; Gaps 3;

QY 15 FMNSEREDCNGEPKRIPEKNSLRQYNSCARLCLNOETVCLASTAMKTENCVAKTK 74
DB 20 FQNTSWEDQJEDNEDSPK-----KNTLWQ----- 42
QY 75 LANTSSMIVPKQKSLASISKEKEKLCVKTFEONSBDQVEFVHLISOMCHYGHINS 134
DB 43 ISNTSVIVSRKKPSRGNYQKEKDLCKYFDQWSESDQVEFVHLISRMCHYGHINS 102
QY 135 YLKEMLRDFTLPAAGLHIAENILSYLDASLCAAEIVCKEWRVTSQMLMKLIE 194
DB 103 YLKEMLRDFTLPAAGLHIAENILSYLDASLCAAEIVCKEWRVTSQMLMKLIE 162
QY 195 RMVETDSLNRGLAERBGWGYLFKNKPPDGNAPPNSFYRALYPIIIDITETESNWRGR 254
DB 163 RMVETDPLMKLSRRRMDQYLFKNRPTDG--PENSRYSLYPIIIDITETESNWRGR 220
QY 255 HSLQRIHCRSETSKGVYCLQYDQKIVSGL 284
DB 221 HNLQRIQCRSENSKGVYCLQYDDEKIIISGL 250

RESULT 15

US-09-213-888-21
; Sequence 21, Application US/09213888A
; Patent No. US20020164683A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Li, Jimie
; APPLICANT: Pauley, Adele M.
; TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
; TITLE OF INVENTION: Encode Them
; FILE REFERENCE: 6142
; CURRENT APPLICATION NUMBER: US/09/213,888A
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged

OTHER INFORMATION: homo sapien
US-09-213-888-21

Query Match 21.2%; Score 644.5; DB 9; Length 626;
Best Local Similarity 30.1%; Pred. No. 5.3e-50;
Matches 169; Conservative 103; Mismatches 222; Indels 67; Gaps 15;

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QY 8 LQEKALKFNNSSEREDCNNGEPKRIIPK--NSLRQ--TNSCARLCLNQETVCLASTA 63
DB 53 MEQKLISEEDLNEMESLGLTMEQKLISEEDLNEMKRLDHSSEVSFSLGKPKCKVSEY 112
QY 64 MKTENCV-----AKTKLANGTSSMTVPKORKLASYEKEKEP--CVKTFEQWSESD 112
DB 113 TSTTGLVPCSAVPTTFEGDLRANQG-----QQRRTITVQPTTGLQEWLKMFGWSGPE 167
QY 113 QVEFEVHLISQWCHQHGINSYKMLORDFITLALPARGLDHIAENIISYLDKSLCNA 172
DB 168 KLALDELIDSCPTQVKMMQVIEPQFORDFISLP---KELALVLSFLEPKDLLQA 223
QY 173 ELVCKEYVYVTSQDGLMKLIERMVRTDSLWRLAE---RRGWQYLFKNKPPDGNAP 227
DB 224 AOTCRVWRLAEDNLMEKEKE-----EGIDELPHIKRK-----VTKPGFIHSP 269
QY 228 PMSFYRALYPKIIODIETIESNMRCGRHSIORIHGRSETSKGVYCIQYDDQKIVSGLRDN 287
DB 270 WKSAY-----IRQ--HRIDTMMRGELKSPKV-LKGDHDVITCQFGCNRIVSGSDN 320
QY 288 TIKIDKNTLECKRIITGHTGSVLCIYDERVIYITGSSDSTVRVWDVNTGEMLNTLIHHC 347
DB 321 TLKWSAVYTGKCLRTLVTGHTGVWSQMRDNIISGSTDRTLKWNNAETGECIHLYGHT 380
QY 348 EAVLHREFNMGMMVYCSKDRSLAVWDMASPTDITLRVLVGHRAVNVVDEDDXYIVSAS 407
DB 381 STVRCHLHKKRVVSGSRDATLRVWDIETGQCL--HVLMGHVAARCVQYDGRRVSGA 437
QY 408 GDRITKVNNTSTCEFRVTLNGHKRGIAQLQYRDLVWSSSDNTIRLMDIECGACLRVLE 467
DB 438 YDFWYKVMDEPETCTCHTLQHTNRYVSLQFDGIHVSSGLDTSIRVWDVEFGNCIHLYT 497
QY 468 GHEELVRCIRFPNKRIVSGAYDGKIKWDLVALDPRAPAGTLCRLTV--EHSGRVFR 524
DB 498 GHQSLTSGMELKDNILVSGNADSTYKIWDIKTG-----QCLQTLQGPKNHQSAYTC 548
QY 525 LQFDEFQIVSSSHDDTILIMD 545
DB 549 LQFNKNFVITSSDDGTIVKLM 569

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Search completed: April 25, 2005, 16:30:31
Job time : 136 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 16:18:52 ; Search time: 42 Seconds

(without alignments)
1303.508 Million cell updates/sec

Title: US-09-415-795-4

Perfect score: 3034
Sequence: 1 MDPRAVIOEAKLKRMNSE.....PAAQAPPPSPRTTYISR 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2597	85.6	518	2	B48088
2	1635.5	53.9	701	2	T16607
3	690	22.7	506	2	T50211
4	590.5	19.5	605	2	T18932
5	545	18.0	640	2	S49932
6	531.5	17.5	650	2	T46660
7	520	17.1	579	2	T22703
8	519.5	17.1	267	2	S62507
9	455.5	15.0	1356	2	T18521
10	453	14.9	775	2	T45136
11	413.5	13.6	1227	2	AB1810
12	399	13.2	779	2	S56245
13	396.5	13.1	703	2	T43557
14	378.5	12.5	1189	2	AI2493
15	375	12.4	1747	2	AC1842
16	374	12.3	1526	2	AC2239
17	373.5	12.3	1258	2	AI2155
18	373.5	12.3	1683	2	AF0071
19	361.5	11.9	677	2	AB1861
20	358.5	11.8	559	2	AB2202
21	354	11.7	409	2	S36113
22	354	11.7	410	2	S48052
23	341	11.2	515	2	S19487
24	339.5	11.2	777	2	T41075
25	337	11.1	1146	2	A55532
26	336	11.1	676	2	AB2195
27	334	11.0	589	2	AG2400
28	333.5	11.0	1711	2	AD1842
29	332.5	11.0	317	2	T46032

30	330	10.9	333	2	G85034	Probable WD-repeat
31	320	10.5	934	2	AG1889	WD-40 repeat prote
32	318	10.5	422	2	A56640	CDG4 repeat unit-c
33	313.5	10.3	376	2	T19266	hypothetical prote
34	312.5	10.3	714	2	S56893	hypothetical prote
35	312	10.3	786	2	AG2375	WD-40 repeat-prote
36	312	10.3	876	2	T51507	WD40-repeat protei
37	307.5	10.1	1693	2	S76086	beta transducin-1i
38	306.5	10.1	598	2	AE2415	WD-repeat protein
39	306	10.1	1189	2	AD2154	WD-repeat protein
40	305	10.1	704	2	S33263	transcription init
41	299.5	9.9	1194	2	T03818	apoptotic proteina
42	298	9.8	265	2	AF1890	WD-repeat protein
43	297.5	9.8	357	2	AI2099	WD-40 repeat prote
44	297	9.8	502	2	T41148	trp-aap repeat con
45	296.5	9.8	304	2	AG1837	WD-40 repeat prote

ALIGNMENTS

RESULT 1

B48088 beta-transducin repeat-containing protein - African clawed frog

N:Alternate names: beta-Trcp

C:Species: Xenopus laevis (African clawed frog)

C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 16-Aug-2004

C/Accession: B48088

R:Spevak, W.; Keiper, B.D.; Stratowa, C.; Caetanon, M.J.

Mol. Cell. Biol. 13, 4953-4966, 1993

A:Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase are

A:Reference number: A48088; MUID:93330289; PMID:8393141

A/Accession: B48088

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-518 <SP>

A:Cross-references: UNIPROT:091854; GB:M98268; NID:G295542; PIDN:AAA02810.1; PID:G295543

C:Superfamily: WD repeat homology

C:Keywords: duplication

F:431-462/Domain: WD repeat homology <WD1>

Query Match	85.6%	Score 2597	DB 2	Length 518
Best Local Similarity	91.6%	Pred. No. 5e-192		
Matches	488	Conservative	7	Mismatches 8; Indels 30; Gaps 1
QY	18	SSEREDCNGGPPRKIIPEKNSLRQTYNSCARLCINQETVCLASTAMTKENCVAATKLAN	77	
DB	13	ASEREDCNRDEPPRKIIPEKNTLRQ-----TKLAN	42	
QY	78	GTSSMIVPKQRKLSASVEKEKELCVKFEQMSSENOVEFVEHLISOMCHYQGHINSYIK	137	
DB	43	GTSSMIVPKQRKLSANVYKEKELCVKFEQMSSENOVEFVEHLISOMCHYQGHINTYIK	102	
QY	138	PMLQRFITLALPARGLDIAENIISYLDKSLCAAEVCCKEYRYTSQGLMKLIERNV	197	
DB	103	PMLQRFITLALPARGLDIAENIISYLDKSLCAAEVCCKEYRYTSQGLMKLIERNV	162	
QY	198	RTDSIMRGLAERRGQYLFXNKPDPGNAFPNSFYRALYPKIIQDIETIESNMRGGRSL	257	
DB	163	RTDSIMRGLAERRGQYLFXNKPDPGKTTPNSFYRALYPKIIQDIETIESNMRGGRSL	222	
QY	258	ORIHRSFSTSGVYGLQYDQKIVSGLRDNITKIMDKNTLECKRIILGHTGSVLQLOYDE	317	
DB	223	ORIHRSFSTSGVYGLQYDQKIVSGLRDNITKIMDKNTLECKRIILGHTGSVLQLOYDE	282	
QY	318	RVIIITGSSDSTVYRVWDVTGEMTLNLIIHCEAVLHLEFNNGMVYCSKDRSIAVDMASP	377	
DB	283	RVIIITGSSDSTVYRVWDVTGEMTLNLIIHCEAVLHLEFNNGMVYCSKDRSIAVDMASA	342	
QY	378	TDITLRRVTVGHRAAVNVVDQDKIVASGDRITKVAWNTSTCEVVRVRLNGHKGIAQLQ	437	
DB	343	TDITLRRVTVGHRAAVNVVDQDKIVASGDRITKVAWNTSTCEVVRVRLNGHKGIAQLQ	402	

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-605 <BAD>
 A:Cross-references: UNIPROT:P87053; EMBL:Z94864; PIDD: CAB08168.1; GSPDB: GN00066; SPDB: SF
 A:Experimental source: strain 972h-, cosmid c57A10
 C:Genetics:
 A:Gene: SPDB:SPAC57A10.05c
 A:Map position: 1
 C:Superfamily: WD repeat homology

Query Match: 19.5%; Score 590.5; DB 2; Length 605;
 Best Local Similarity 29.0%; Pred. No. 1.9e-37;
 Matches 156; Conservative 86; Mismatches 189; Indels 107; Gaps 12;

QY 80 SSMIVPKQKLSASVEKEKELCVKFEQKSE---SDQVEFVHLISQMHYGHINSL 136
 DB 46 SSM---HNEISGLSEKSRQVEAWAFAFEASCSEKRLAQIINSSSSLSFASSTL 101
 QY 137 KPMLODFITALPARGLDHIAENILSYLDAKSLCAAEIVCKEYRVTSQMLMKLIERM 196
 DB 102 DSLVLDLPLSLPV---EISFRILSPIDARSLQQAQVSKMKELADDDVIVHMCQEH 157
 QY 197 VRTDLSLWGLAERRGQVLFKN----- 219
 DB 158 INRK-----CEKCGMGLPLERNTLYAAKASIQKRYERLTRGVDAQHESSPVKKALD 211
 QY 220 -----KPPDGNAPPNSF-----YALPPIKIIQDIETTESMWRGGRHSIQ 258
 DB 212 DYPSSNEBETISSVPPSPNSDSKFFLPKTRPMKRYEAERCR---VECMWRHR----- 263
 QY 259 RIHGR-----SETSKVYVCLQYDDQKIVSGLRDNTIKIMDKTLECKRIITGHTSVLCIQ 314
 DB 264 ---CQOVLVSGHSDVQMCQIVRNILASGSYDATTIRLMNLTAFQOVALLEGHSSVTCIQ 320
 QY 315 YDERVIITGSSDSTVRVDVNTGEMLNTLIHCEAVLHLRFNNGMVTCSKDRSIAVDM 374
 DB 321 FDQCLTIGSMDKTRIRNMVYRSECSILHGHSTSVLCITFPSTLLVSGSADCTVKLMHF 380
 QY 375 ASPDITLRVLVGRRAVNVDF--DDKIVASAGDRTIKVWNTSTCEFTVTLNGHKRG 432
 DB 381 SGGKRITLR---GHTGPNVSVRIIRDGLVYSGSDSTIKIWSLETWYCLHTFPAHIGP 436
 QY 433 IACIQYRRLVAVSGSDNTIRLMDIECGACLRVLBSGHELVLCIRFDMKRIYVSGADGI 492
 DB 437 VQSLADSLRPLSCGLDGTIKOMDIEKKCVHTLFGHIEGWELIADHRLISGADGVV 496
 QY 493 KVMDLVAALDPRAPAGTLCRLTVLHSGRVFRLQDFEQIVSSSHDDTILLWDFLNDP 550
 DB 497 KVMACE-----CVHTLKNHSEPVTSVALGDCEVVGSGSDGKIYLMFLNNAP 543

RESULT 5

ME730 protein - yeast (Saccharomyces cerevisiae)
 S49932
 N:Alternate names: protein Y19905.02; protein Y11046w
 C:Species: Saccharomyces cerevisiae
 C>Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 16-Aug-2004
 C:Accession: S49932; S43750
 R:Odell, C.; Bowman, S.
 submitted to the EMBL Data Library, December 1994
 A:Reference number: S49931
 A:Accession: S49932
 A:Molecule type: DNA
 A:Residues: 1-640 <ODS>
 A:Cross-references: UNIPROT:P39014; GB:Z47047; EMBL:Z46061; NID:G603997; PID:G763300; MI
 R:Thomas, D.; Cherest, H.; Barbey, R.; Sudin-Kerjan, Y.
 submitted to the EMBL Data Library, December 1993
 A:Reference number: S43750
 A:Accession: S43750
 A:Molecule type: DNA
 A:Residues: 1-60, 'I', 62-640 <THO>
 A:Cross-references: EMBL:L26505; NID:G432493; PID:G432494
 C:Genetics:

A:Gene: SGD:ME730
 A:Cross-references: SGD:S0001308; MIPS:Y11046w
 A:Map position: 9L
 C:Superfamily: WD repeat homology
 F:298-329/Domain: WD repeat homology <WD1>
 F:338-369/Domain: WD repeat homology <WD2>
 F:374-409/Domain: WD repeat homology <WD3>
 F:417-450/Domain: WD repeat homology <WD4>

Query Match: 18.0%; Score 545; DB 2; Length 640;
 Best Local Similarity 28.9%; Pred. No. 6.6e-34;
 Matches 167; Conservative 85; Mismatches 202; Indels 124; Gaps 17;

QY 34 IPEKSLAQITNSCARCLLN-QETVCLASTMKTEHCVAK-TKLANGSSMIVPKQKLS 91
 DB 86 LPEINFTFCYRHNPDIFSPHTHACYKODLKRTOEINANIAKPLQEOQSDIHIIISKYS 145
 QY 92 ASYEKEKELCVKFEQKSESDQVEFVHLISQMHYGHINSLYKPMLODFITALPAR 151
 DB 146 NSNDKIRKL-----ILDGILSTSCFPQSLSYSLVTHMIKIDFISILP-- 188
 QY 152 GLDHIENILSYLDAKSLCAAEIVCKEYRVTSQMLMKLIERMVRTDSLRGLAERR- 210
 DB 189 --QELSLKILSYLDQOSLCNATRVCRKQKXLADDDRVVYHMCQEH-----DRKC 236
 QY 211 ---GMGOVLFKNK-----PPDGNAPNSFYALPPIKIIQDIETTESMWRGGRHSIQ 258
 DB 237 PNCGMGLPLHMKRARIQONSTGSSSNADIQOTTRPKVIVYERFVKESSNRKG----- 291
 QY 259 RIHGRSEFSK---GVYCLQYDDQKIVSGLRDNTIKIMDKTLECKRIITGHTSVLCIQ 314
 DB 292 --HCRIOGFKGMQVLLQGFYRNLPLFTGYSVSTIGIWDLTGKLIIRLSGHSDDVTKLY 349
 QY 315 YDERVIITGSSDSTVRVDVNTGEMLNTLIHCEAVLHLRFNNGMVTCSKDRSIAVDM 374
 DB 350 FDDRKLITGSLDKTRVNMVYITGECISTYRGHSVLSVDSYQKIVYSGSADKTVKVMHV 409
 QY 375 ASPDITLRVLVGRRAVNVDFPDDKI--VSASGDRTIKVWNTSTCEFTVTLNGH--- 429
 DB 410 ESRCTYTLR---GHTGVNVCVKLHPKSPSCPSGDDTTIRMDIRITNSCLKVFRGHVQ 465
 QY 430 KRGIAQLQYRD--RLVSGSS----- 448
 DB 466 VQKIIPILTIKVENLATNTSDGSSPODDPTMTGADSDTPNSQETVLDENIYPPHIL 525
 QY 449 -----DNTIRLMDIECGACLRVLBSGHELVLCIRFDMKRIYVSGAYDGKIKVMDLVAALDP 503
 DB 526 LSCGIDNTIKIMDVYTGKCIKRTQFGHVGWMDIADNFRITSGSHDSIKVMDLQSG--- 582
 QY 504 RAPAGTLCRLTVLHSGRVFRLQDFEQIVSSSHDDTI 541
 DB 583 ---KCMHTF---NGR--RLQRETOHTOTQSLGDKV 609

RESULT 6

T46660
 sulfur controller-2 protein [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 16-Aug-2004
 C:Accession: T46660
 R:Kumar, A.; Paletta, J.V.
 Proc. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995
 A:Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a
 A:Reference number: T23121; MUID:95241499; PMID:7724564
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-650 <KUM>
 A:Cross-references: UNIPROT:O01277; EMBL:U17251; NID:G806757; PIDD:AAA68968.1; PID:G8067
 C:Genetics:
 A:Gene: scon-2
 A:Map position: 3
 A:Introns: 75/3; 319/1; 354/1

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C/Accession: AB1810
R/Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Saemoto, S.; Watanabe, A.; Iriuchih
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AB1810
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1227 <KUR>
A/Cross-references: UNIPROT:Q820R1; GB:BA000019; PIDN:BA077553.1; PID:q17135007; GSPDB:Q
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr0029

Query Match 13.6%; Score 413.5; DB 2; Length 1227;
Best Local Similarity 23.9%; Pred. No. 2.2e-23;
Matches 140; Conservative 114; Mismatches 208; Indels 125; Gaps 22;

QY 10 EKALKFNNSSERE-----DCNNGEPKRIIEKXSLKQTYNSCARLCLNQTVCIA 60
DB 378 EKKVYSLGANREYVSFRELKDDMLTTPSPKIMWALSLLR-----RSLIEKASPTLI 431
QY 61 STAMTENCVAATKLANGTSSWIVPKOKRLASYEKELCVKPEQMSQDVEFVHL 120
DB 432 EKASSTQGEKAKSSKFLGESVVM--EYTKAFIENS-----LEESQTKLDF---- 478
QY 121 ISQCHYGHGINSYKLPMLQDFITLAPAGLDHIAENIISYLDKSLCAAEIVCKEMY 180
DB 479 -----INTY--PLMK-----ARSLDYI----- 493
QY 181 RYTSQMLMKLIEEMVNTDSIMRGLARRGCGQLFKKPPDGNAPPN--SFYRALYK 238
DB 494 FOIQERLLIEPVKQKLINIFTELEHLRLMGLTVQCKPPLPKGYAAGNLINLRLQQLD 553
QY 239 IIODETIESN-----WRGGRSL--QRHCRS-----ETSKGVCLQY--D 276
DB 554 KIPDSPPIDLSGRDPSGLTIWQAYFKEYKLETIRANSBDLGSVTEHMSVSVKFSPPD 613
QY 277 DQKIVSGRDNITKIMDKNLTCKKRIITGHTGSLCLQY--DERVIITGSSDSTYVWDV 334
DB 614 GKYPATGLMNGEIRILMQTSNDKQIRIYKGTAMVWAFSPDSRLMASGSADSTIKLMDV 673
QY 335 NTGEMNLTLIHCEAVLHLRF--NNGMWTGCKDSIAVMDASPTDITLRVLYVGHAA 392
DB 674 HTGECLEKTLKNTKRYSVAFSPDGRILASASQDOTIKLMDIATG--NCQOTLIGHDDW 730
QY 393 VVVVDF---DDK--YIVASGDRITIKVNTSTCFEVRTLNHGRKGIACLOYR--DRLV 444
DB 731 VMSVTFSPYDTRDRLILLASSADQHIKLMVATGKCLTKLKGHTREHNSVSFSPGQTILA 790
QY 445 SSSDNITRLMDIECGACLRVLEGHELVRCIRF--DNKRIYSGAYDGKIKVMDVLAALD 502
DB 791 SSGEDSTYRLMDVTKGCGQIPEGHSKRYSVFSPDQOTILASCEDSIRIKLMDIQRG-- 848
QY 503 PPAAPAGTLCRTLVESHSGRVRLQF--DEFOIVSSSHDTIILNPL 547
DB 849 -----ECVNTLMGHSSQVMAIAPSPGRTILISCSDDQTARLMDVI 888

RESULT 12
S56245
cell division control protein CDC4 - yeast (Saccharomyces cerevisiae)
N/Alternate names: protein YFL009w
C/Species: Saccharomyces cerevisiae
C/Date: 02-Sep-1995 #sequence_revision 12-Apr-1996 #text_change 16-Aug-2004
C/Accession: S56245; S48310; A26867; S62304
R/Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasauma, S.I.; Saeau
Submitted to the EMBL Data Library, May 1995
A/Description: Analysis of the nucleotide sequence of chromosome VI from Saccharomyces ce
A/Reference number: S56186
A/Accession: S56245

A/Molecule type: DNA
A/Residues: 1-779 <MR>
A/Cross-references: UNIPROT:P07834; EMBL:D50617; NID:9836685; PIDN:BA09229.1; PID:d1093
R/Churcher, C.
Submitted to the EMBL Data Library, September 1994
A/Reference number: S48310
A/Accession: S48310
A/Molecule type: DNA
A/Residues: 1-579 <CHU>
A/Cross-references: EMBL:Z46255; NID:9559925; PIDN:CMA6341.1; PID:9559926; MIPS:YFL009w
R/Rycohen, J.; Byers, B.
J. Mol. Biol. 195, 233-245, 1987
A>Title: Structural comparison of the yeast cell division cycle gene CDC4 and a related i
A/Reference number: A26867; MUID:88011240; PMID:3309335
A/Accession: A26867
A/Molecule type: DNA
A/Residues: 1-459, 'E', 461-779 <YOC>
A/Cross-references: EMBL:X05625; NID:93502; PIDN:CMA29113.1; PID:93503
R/Murakami, Y.
Submitted to the EMBL Data Library, April 1994
A/Reference number: S62302
A/Accession: S62304
A/Molecule type: DNA
A/Residues: 1-779 <MDW>
A/Cross-references: EMBL:D31600; NID:9836814; PIDN:BA06495.1; PID:d1007066; PID:9836815
C/Genetics:
A/Gene: SGD: CDC4
A/Cross-references: SGD:S0001885; MIPS:YFL009w
A/Map position: 6L
C/Function:
A/Description: Initiation of DNA replication; separation of the spindle pole bodies to f
C/Superfamily: WD repeat homology
C/Keywords: cell cycle control
F:458-494/Domain: WD repeat homology <WD1>
F:628-659/Domain: WD repeat homology <WD2>

Query Match 13.2%; Score 399; DB 2; Length 779;
Best Local Similarity 24.3%; Pred. No. 1.5e-22;
Matches 139; Conservative 80; Mismatches 196; Indels 156; Gaps 20;

QY 56 TVCLASTAMTENCVAATKLANGTSSMIVPKOKRLASYEK-----ELCVKYEQW 108
DB 194 TTPLAKTKTTKINN-----NNNIADLIESKDSIISPEYLSDEFSAINNMLPHAYFK-- 244
QY 109 SESQVEFVHLISQCHYGHGINSYKLPMLQDFITLAPARLDHIAENIISYLDKSL 168
DB 245 -----NLFLVLANMRSELSDGLTIKONLKDILTSLPF---EISLKFNYLQPED 294
QY 169 LCAAEIVCKEYR--VTSQMLMKLI--ERWVRTDSIMRGLARRGCGQLFKKPPDGN 225
DB 295 IINSLGYSQNNKTIIRKSTSLMKLLISENFV-----SPKGF 331
QY 226 APPNSFYRALYPKIIQD-----IET--IESNRCGRHSLQRIHCSSETSKGVCLQYD 276
DB 332 NSLMLKLSQKPKLSQDRLSLFLENIFILKMNYPKFPVQRTLLGHMTSVITCLQFE 391
QY 277 DQKIVSGRDNITKIMDKNLTCKKRIITGHTGSLCLQYDE-RVIITGSSDSTYVWDV 335
DB 392 DNYVITGADDMKIVVYSINKFLLQLSGHDGVAWKYAHAGILVSGSTDRIVRWDIK 451
QY 336 TGEMLNLTLIHCEAVLHLRFNNGMWTGCKDSIAVMDASPTDITLRVLYVGHAAVNV 395
DB 452 KG-----CCT-----HVPKGNSTVRC 468
QY 396 VDFPD---KYIVASGDRITIKVNT-----STCE-----FVRTLNG 428
DB 469 LDIVYKNIKIVYSGRDNITLHWKLPKSESSVPDGHEDVPLVFHTPEENPYFVGVLRG 528
QY 429 HKRGIAQLQYDRVLVSGSSNTIRLMDIECGACLRVLEGHELVRCIRPN--KRIYSG 486
DB 529 HMAVRYTSGHGNIVSGSYDNTLIVDWQMKCLYLISGHTDRIYSTIYHERKRCISA 588
QY 487 AYDGKIKVMDL-----VAALDPAPAGTLL--CLRTLVESHSGRVRLQFDEFOIVSS 535

Db 589 SMDTIRIWDLENIMNNGECYATNSASPCAKILGMATYLLQGHETALVELLRISDKRYLSA 648
 QY 536 SHDDTILTWDFLNDPAQAQEPSPRSTTTY 566
 Db 649 AADGSGIRGWD-AND-----YSRKEST 668

RESULT 13

T43557
 F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: proteolysis factor sud1p
 C:Species: Schizosaccharomyces pombe
 C:Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T43557; T43794; T43798
 R:Wolf, D.A.; Jackson, P.K.

submitted to the EMBL Data Library, December 1997
 A:Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in cell cycle regulation.
 A:Reference number: Z22576
 A:Accession: T43557

A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA

A:Residues: 1-703 <WOL>

A:Cross-references: UNIPROT:O14170; EMBL:AF038667; PIDN:AAB95480.1

A:Experimental source: strain h-972

R:Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, August 1996

A:Reference number: Z21812

A:Accession: T38794

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-703 <GEN>

A:Cross-references: EMBL:Z98602; PIDN:CA811275.1; GSPDB:GN00066; SPDB:SPAC4D7.03

A:Experimental source: strain 972h; cosmid c4D7

R:Juliepel, P.V.; Tien, D.; Kelly, T.J.

Proc. Natl. Acad. Sci. U.S.A. 95, 8159-8164, 1998

A:Title: Sud1+ targets cyclin-dependent kinase phosphorylated Cdc18 and Rum1 proteins for ubiquitination.

A:Reference number: Z22686; MUID:98318628; PMID:9653157

A:Accession: T43798

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-703 <JAL>

A:Cross-references: EMBL:AF064515; NID:g3293382; PIDN:AAC39496.1; PID:g3293383

C:Genetics:

A:Gene: pop2; sud1; SPAC4D7.03

A:Map position: 1

C:Function:

A:Description: required to prevent spontaneous re-replication

Query Match 13.1%; Score 396.5; DB 2; Length 703;
 Best Local Similarity 23.3%; Pred. No. 26-22;
 Matches 146; Conservative 92; Mismatches 226; Indels 163; Gaps 25;

QY 14 KFNSSERED-CNNGEPRKI-----IPEKSLRQTVNSCARLCL---NQETVCL 59

Db 96 KFNSEIENVSYCLDHPSPDVPDPSPISLVQKRF--YSHSLSPKIIISIDRRNRKID 154

QY 60 ASTAMKTECAKYKLANGTSMIVPKQKLSASTEK-EKELCVYFEOWSSDVEFE 118

Db 155 NSISNSNFPSPKPV--DTSNTVSPGSKPISSEDEDLNLSIQTFEDLPFGIO-SYAF 211

QY 119 HLISQMGYOHGH-INSYKLPMLQDPTIALPARGDHAENILSYLAKSICAEALVCK 177

Db 212 FQLMSCKRQSKRLINCEPLKQDILSNLPF---STVOSILNLDHSLSCRLVSP 267

QY 178 EMYRV---TSDGMLMKKLIEMVVRTDLSMGLAERGGQYLFPNKKPPDGANP---N 229

Db 268 TWNRILDVHTS--YMKMF-----SLFGQINENMW---KYAPNMLNRPFLIND 312

QY 230 SFYRLAYPKIIDIITISNMFGRHSLSR----- 259

Db 313 QISDDYFPEIFK-----RHFLNRKRWLPSPISIPSHLSPIHVNFMITSLHL 360

QY 260 -----IHCSETSK-GVYCLQDDQKIVSGLRDNTIKIWDKNT 296
 Db 361 KDRITTTGSGGTIOHNAITGLVLEARLBQHKQGVAAVKHNTLVSGSIDKTVRVNNIK 420
 QY 297 IECKRIILGHTGSLVCLQY-----DERVIITGSSDSITVAVDVTGEML 340
 Db 421 AKCTHIFRGHISIIIRCLLEIVPSRLIRGVETVEPDPQYIVSGSRDRLRV----- 472
 QY 341 NTLHHCEAVLHLRRNMGMTCSKDRSIAVDMASPDIDITRLVLRVGRRAVNVDFPD 400
 Db 473 -----KLPNTPDPYLPDNTNSIDRWE-KNPFV--HTLIGHITDSVTRTISGVG 517
 QY 401 KYIVASGDRITKVNNTSTCEFRVTLNGHKRGIACLOYRD--RLVVGSSDNTIRLMDIE 458
 Db 518 DILVSGSDSSIRIRVSTGECTYLHGRHSRLRYVLYEPENNTICSGMSDSIRYMDIS 577
 QY 459 CGACLRVLEHGEHLVRCIRFDRKIRVSGAYDQKIKVMDLVVALDPRAPAGTLCLRTLYEH 518
 Db 578 TGTCKYVLEGHDAFYTLLNVPQNRLISGSADSTIRIWD---LNTGKP-----LMVLPDN 628
 QY 519 SGRVRLQDFERQIVSSSHDITLIWD 545
 Db 629 SGYISSFVSDERKTI-SGNDGSVKLMD 654

RESULT 14

WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid PCC7120alpha

AT2493

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AT2493

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Saemoto, S.; Watanabe, A.; Iritiguchi, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AT2493

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1189 <KUR>

A:Cross-references: UNIPROT:O8VLE09; GB:BA000020; PIDN:BA878213.1; PID:g17135667; GSPDB:G

C:Genetics:

A:Gene: at7129

A:Genome: plasmid

Query Match 12.5%; Score 378.5; DB 2; Length 1189;
 Best Local Similarity 26.7%; Pred. No. 1e-20;
 Matches 96; Conservative 63; Mismatches 107; Indels 93; Gaps 10;

QY 280 IVSGLRDNTIKIWDKNTLECKRIILGHTGSLVCLQYD--ERVIIITGSSDSITVAVDVTG 337

Db 745 LASGSFDQNVMLDHTGKCVMTLQHGTVTSVAFNPKMULLSGSYDQSVKVDKRTG 804

QY 338 EMNLTLHHCBAVHLARN----- 356

Db 805 RCLDTLKRGHTRINISVAFHPQGLFVSGDDHAAKIMELGTGQCIKTFOGSHNATYTTAH 864

QY 357 ---NGMWTYCKDRSIAVDM--MASPTDITLR---RVLVGRRAVNVDFPD--KYIVS 405

Db 865 NWEHSLASGHEDQIKIMDLNLSPHKSNVNTFRILQGHSNRVSFVSSTGQLLAS 924

QY 406 ASGDRITKVNNTSTCEFRVTLNGHKRGIACLOYR--DLVVGSSDNTIRLMDIEGAC 463

Db 925 GSADRTITLMSPHGTQCLHTLHGSGVWMAIAFSDDKLASGYDHTVKIMDVSSGCL 984

QY 464 RVLGHEHLVRCIRF--DNKRIVSGAYDQKIKVMDL-----VAALDP 503

Db 985 QTLQHPESVLAIVASCDGKTLFSSGYKLVKQMDVETGYCLQTEWADSNNVMAVAASRD 1044

QY 504 RAPAGT-----LCRLTVESHSGRVRLQF--DEFQIVSSSHDDITLIWD 545

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 25, 2005, 16:27:33 ; Search time 179 Seconds

(without alignments)
1627.782 Million cell updates/sec

Title: US-09-415-795-4

Perfect score: 3034
Sequence: 1 MDPAAVLAQEKALKFPMNSE.....PAAQAEPSPSPRTTYTISR 569

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3006	99.1	605	1	FWIA_HUMAN	Q9Y297 homo sapien
2	2997	98.8	569	2	Q9OU15	Q9OU15 mus musculu
3	2990	98.5	569	2	Q9Z159	Q9Z159 mus musculu
4	2978	98.2	569	2	Q9R1G7	Q9R1G7 mus musculu
5	2821	93.0	564	2	Q6BDS0	Q6BDS0 homo sapien
6	2597	85.6	518	1	TRCB_XENLA	Q91854 xenopus lae
7	2395	78.9	529	2	Q8BY90	Q8BY90 mus musculu
8	2384.5	78.6	542	1	FWIB_HUMAN	Q9UKB1 homo sapien
9	2380	78.4	563	2	Q8KO22	Q8KO22 mus musculu
10	2360	77.8	555	2	Q8CHD5	Q8CHD5 mus musculu
11	2286	75.3	563	2	Q9Z3H0	Q9Z3H0 mus musculu
12	2258.5	74.4	527	2	Q6PGM4	Q6PGM4 brachydanio
13	2250	74.2	527	2	Q7ZVZ1	Q7ZVZ1 brachydanio
14	2128	70.1	621	2	Q8CSD3	Q8CSD3 ciona intest
15	2089.5	68.9	510	2	Q44382	Q44382 drosophila
16	2089.5	68.9	510	2	Q9VDE3	Q9VDE3 drosophila
17	1948.5	64.2	555	2	Q7PYH7	Q7PYH7 anopheles g
18	1638.5	54.0	665	1	LI23_CAEEL	Q09990 caenorhabdi
19	1498	49.4	430	2	Q9BJS4	Q9BJS4 heterodera
20	1230	40.5	252	2	Q9Z2C7	Q9Z2C7 mus musculu
21	690	22.7	506	1	POFB_SCHPO	Q09855 schizosacch
22	675.5	22.3	1083	2	Q7Q7E2	Q7Q7E2 anopheles g
23	661	21.8	1326	2	Q9VZF4	Q9VZF4 drosophila
24	640	21.1	707	1	FBW7_HUMAN	Q9VZF4 drosophila
25	639	21.1	629	1	FBW7_MOUSE	Q9VZF4 drosophila
26	638	21.0	122	2	Q8UTN3	Q8UTN3 xenopus lae
27	621.5	20.5	755	2	Q7S199	Q7S199 xenopus lae
28	618.5	20.4	520	2	Q6COT5	Q6COT5 yarrowia li
29	590.5	19.5	605	1	POPI_SCHPO	Q6COT5 yarrowia li
30	583	19.2	1010	2	Q7RMG8	Q7RMG8 neurospora
31	575	19.0	678	1	SCOB_EWENTI	Q00659 emericella

32	556	18.3	569	2	Q7SAK9	Q7SAK9 ashyba gosa
33	545.5	18.0	623	2	Q6C1D5	Q6C1D5 klyveromyc
34	545	18.0	640	1	MTJ0 YEAST	P39014 saccharomyc
35	541.5	17.8	667	2	Q6BRQ3	Q6BRQ3 debaryomyc
36	539.5	17.8	741	2	Q6BM92	Q6BM92 debaryomyc
37	531.5	17.5	650	1	SC02 NEUCR	Q01277 neurospora
38	527	17.4	673	2	Q6FLT6	Q6FLT6 candida gla
39	520	17.1	587	1	SE10 CAEEL	Q93794 caenorhabdi
40	514	16.9	581	2	Q6CHE8	Q6CHE8 yarrowia li
41	503	16.6	1029	2	Q7S2D9	Q7S2D9 neurospora
42	489.5	16.1	650	2	Q7RYJ1	Q7RYJ1 neurospora
43	477.5	15.7	684	1	CDCA CANAL	P53699 candida alb
44	469	15.5	1376	2	Q8X1P2	Q8X1P2 podospora a
45	468.5	15.4	698	2	Q6C5T6	Q6C5T6 yarrowia li

ALIGNMENTS

RESULT 1	FWIA HUMAN	STANDARD	PRT	605 AA.
AC	Q9Y297; Q9Y213;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	F-box/WD-repeat protein 1A (F-box and WD-repeats protein beta-TTCP)			
DE	(E3RSIKappab) (pikappabalpha-E3 receptor subunit).			
GN	Name=BTRC; Synonyms=BTRCP, FBW1A, FBXW1A;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;			
RA	Varon A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,			
RT	Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y., Richard V.,			
RT	"Identification of the receptor component of the IkappaBalpha-			
RT	ubiquitin ligase."			
RL	Nature 396:590-594(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISUE=Lymphoid;			
RX	MEDLINE=98325370; PubMed=9660940; DOI=10.1016/S1097-2765(00)80056-8;			
RA	Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,			
RA	Thomas D., Strebel K., Benarous R.;			
RT	"A novel human WD protein, h-beta-TTCP, that interacts with HIV-1 Vpu			
RT	connects CD4 to the ER degradation pathway through an F-box motif."			
RL	Mol. Cell 1:565-574(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RX	MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;			
RA	Cenciarelli C., Chiau D.S., Guardavaccaro D., Parks W., Vidal M.,			
RA	Pagano M.;			
RT	"Identification of a family of human F-box proteins."			
RL	Curr. Biol. 9:1177-1179(1999).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISUE=Brain;			
RX	MEDLINE=22388957; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,			
RA	Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diachenko L., Marulian K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,			
RA	Bromberg M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosch S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[5]
RN CHARACTERIZATION.
RP MEDLINE=99145464; PubMed=9990852;
RA Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Ellledge S.J.,
RA Harper J.W.;
RT "The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
RT with phosphorylated destruction motifs in I-kappa-B-alpha and beta-
RT catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
RL Genes Dev. 13:270-283 (1999).
[6]
RN INTERACTION WITH UBQLN1.
RP TISSUE=B-cell;
RX MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
RA Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
RA Kedersta N.L., Gill G., Howley P.M.;
RT "The hPLIC proteins may provide a link between the ubiquitination
RT machinery and the proteasome.";
RL Mol. Cell 6:409-419 (2000).
[7]
RN INTERACTION WITH PHOSPHORYLATED CTNNB1.
RP MEDLINE=22072105; PubMed=12077367;
RX Sadot E., Conacci-Sorrenti M., Zhurinsky J., Shitzer D., Lando Z.,
RA Zharhary D., Kam Z., Ben-Zeev A., Geiger B.;
RT "Regulation of S33/S37 phosphorylated beta-catenin in normal and
RT transformed cells.";
RL J. Cell Sci. 115:2771-2780 (2002).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
RP AND CTNNB1.
RX MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X;
RA Wu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W.,
RA Pavletich N.P.;
RT "Structure of a beta-TrCP1-Skp1-beta-catenin complex: destruction
RT motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
RT ligase.";
RL Mol. Cell 11:1445-1456 (2003).
-!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F-
-!- box protein) ubiquitin ligase complex, which mediates the
-!- ubiquitination of proteins involved in cell cycle progression,
-!- signal transduction and transcription. Regulates the stability of
-!- CTNNB1 and participates in Wnt signaling.
-!- PATHWAY: Ubiquitin conjugation; third step.
-!- SUBUNIT: Interacts directly with SKP1 in the SCF complex.
-!- Interacts specifically with phosphorylated CTNNB1 and NFKBIA,
-!- ubiquitination substrates. Binds UBQLN1.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
-!- Event=Alternative splicing; Named isoforms=2;
-!- Name=1;
-!- IsoId=Q9Y297-1; Sequence=Displayed;
-!- Name=2;
-!- IsoId=Q9Y297-2; Sequence=VSP_006764;
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 7 WD repeats.

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CC EMBL; AF101784; AAD08702.1; -.
CC EMBL; Y14153; CAA74572.1; -.

DR EMBL; AF129530; AAF04464.1; -.
DR EMBL; BC027994; AAH27994.1; -.
DR PDB; 1P22; X-ray; A=171-605.
DR Genew; HGNC:1144; BIRC.
DR MIM; 603482; -.
DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR008945; Skp1_Skp2.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR01046; WD40_1like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
DR 3D-structure; Alternative splicing; Ligase; Repeat;
DR Ub1 conjugation pathway; WD repeat; Wnt signaling pathway.
DR DOMAIN
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FT REPEAT 20502 20540
FT REPEAT 20540 20578
FT REPEAT 20578 20616
FT REPEAT 20616 20654
FT REPEAT 20654 20692
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FT REPEAT 21946 21984
FT REPEAT 21984 22022
FT REPEAT 22022 22060
FT REPEAT 22060 22098
FT REPEAT 22098 22136
FT REPEAT 22136 22174
FT REPEAT 22174 22212
FT REPEAT 22212 22250
FT REPEAT 22250 22288
FT REPEAT 22288 22326
FT REPEAT 22326 22364
FT REPEAT 22364 22402
FT REPEAT 22402 22440
FT REPEAT 22440 22478
FT REPEAT 22478 22516
FT REPEAT 22516 22554
FT REPEAT 22554 22592
FT REPEAT 22592 22630
FT REPEAT 22630 22668
FT REPEAT 22668 22706
FT REPEAT 22706 22744
FT REPEAT 22744 22782
FT REPEAT 22782 22820
FT REPEAT 22820 22858
FT REPEAT 22858 2289

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FT      TURN      476      477
FT      STRAND      478      483

Query Match      99.1%; Score 3006; DB 1; Length 605;
Best Local Similarity 94.0%; Pred. No. 1,2e-217;
Matches 569; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY      1 MPAEAVLOEKALKFM-----NSSRREDC 24
DB      1 MPAEAVLOEKALKFMCSMPRSIMWLGCSLADMSRLCLVNPFGALTAFONSSREDC 60

QY      25 NNGEPPRKIIPEKNSLRQTYNSCARLCLNOETVCLASTAMKTENCVAKTLANGTSSMTV 84
DB      61 NNGEPPRKIIPEKNSLRQTYNSCARLCLNOETVCLASTAMKTENCVAKTLANGTSSMTV 120

QY      85 PKORKLASYEKEKELCVKFEQWSESDOVEFEHLISQMCHYOHGHINSYKPMLOQDF 144
DB      121 PKORKLASYEKEKELCVKFEQWSESDOVEFEHLISQMCHYOHGHINSYKPMLOQDF 180

QY      145 ITALPARGLDHIAENILSYLDAKSLCAAEVCKEWRVTSDDMLMKLIERVVRTDSLMR 204
DB      181 ITALPARGLDHIAENILSYLDAKSLCAAEVCKEWRVTSDDMLMKLIERVVRTDSLMR 240

QY      205 GLAERBGMOYLFXKKNPPDGNAPNSFYALYPKIIODIETIESNWRGSHLQRIHCRS 264
DB      241 GLAERBGMOYLFXKKNPPDGNAPNSFYALYPKIIODIETIESNWRGSHLQRIHCRS 300

QY      265 ETSKGVYCLQYDDQKIVSGLRNTIKIKMDKTLCKRILITGTVSVLCQYDERVITGS 324
DB      301 ETSKGVYCLQYDDQKIVSGLRNTIKIKMDKTLCKRILITGTVSVLCQYDERVITGS 360

QY      325 SSTSTRVMDVNTGEMLNTLIHCEAVLHIFENNGMVTSCKRSIAVMMASPTDITLR 384
DB      361 SSTSTRVMDVNTGEMLNTLIHCEAVLHIFENNGMVTSCKRSIAVMMASPTDITLR 420

QY      385 VLVGRRAAVNVDPDDKYIVSASGRTIKVMNTSTCEFYRTINGHKGRIACIQYDRILV 444
DB      421 VLVGRRAAVNVDPDDKYIVSASGRTIKVMNTSTCEFYRTINGHKGRIACIQYDRILV 480

QY      445 SSSSNTTRLMIDIEGACLRVLEGHEBELVRCIRFPNKRIVSAYDGKIKVMDLVALDPR 504
DB      481 SSSSNTTRLMIDIEGACLRVLEGHEBELVRCIRFPNKRIVSAYDGKIKVMDLVALDPR 540

QY      505 APAGTLCRTIYHSGRVRLQDFEROIVSSSHDPTLIMDLNPAQAEPSPRSRTY 564
DB      541 APAGTLCRTIYHSGRVRLQDFEROIVSSSHDPTLIMDLNPAQAEPSPRSRTY 600

QY      565 TYISR 569
DB      601 TYISR 605

RESULT 2
O9QUT5      PRELIMINARY;      PRT;      569 AA.
AC      O9QUT5:
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Ubiquitin ligase FWD1 (Beta-TCP protein E3RS-IkappaB) (F-box-WD40
       repeat protein 1) (Beta-transducin repeat containing protein).
GN      Name=Btrc; Synonyms=Fbxw1;
OS      Mus musculus (Mouse);
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99199275; PubMed=10097128; DOI=10.1073/pnas.96.7.3859;
       Hatakeyama S., Kitagawa M., Nakayama K., Shitane M., Matsumoto M.,
       Hatori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.,
       Nakayama K.-I.;
       "Ubiquitin-dependent degradation of IkappaBalpha is mediated by a

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RT      ubiquitin ligase Skp1/Cul 1/F-box protein FWD1.";
RL      Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99075339; PubMed=9859996; DOI=10.1038/25159;
       Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
       Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
       "Identification of the receptor component of the IkappaBalpha-
       ubiquitin ligase.";
       Nature 396:590-594(1998).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/Sv;
RX      MEDLINE=21601157; PubMed=11735228; DOI=10.1006/geno.2001.6658;
       Maruyama S., Hatakeyama S., Nakayama K., Ishida N., Kawakami K.,
       Nakayama K.-I.;
       "Characterization of a mouse gene (Fbxw6) that encodes a homologue of
       Caenorhabditis elegans SEL-10.";
       Genomics 78:214-222(2001).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CZECH II; TISSUE=Mammary tumor;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
       Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
       Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
       Altschul S.F., Zeeberg B., Buetow K.H., Scheefel C.F., Bhat N.K.,
       Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
       Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
       Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Prange C.,
       Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
       Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullighan J.,
       Boeck S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
       Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
       Villalón D.K., Muzny D.M., Sodergren E.D., Lu X., Gibbs R.A.,
       Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
       Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
       Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
       Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
       Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
       Jones S.J., Marra M.A.;
       "Generation and initial analysis of more than 15,000 full-length human
       and mouse cDNA sequences.";
       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [5]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CZECH II; TISSUE=Mammary tumor;
RX      Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
RL      -1- SIMILARITY: Contains 7 WD repeats.
CC      -1- SIMILARITY: Contains 7 WD repeats.
DR      EMBL, AF081887; AAD17755.1; -.
DR      EMBL, AF099932; AAD08701.1; -.
DR      EMBL, AF391190; AAL40929.1; JOINED.
DR      EMBL, AF391178; AAL40929.1; JOINED.
DR      EMBL, AF391179; AAL40929.1; JOINED.
DR      EMBL, AF391183; AAL40929.1; JOINED.
DR      EMBL, AF391184; AAL40929.1; JOINED.
DR      EMBL, AF391185; AAL40929.1; JOINED.
DR      EMBL, AF391186; AAL40929.1; JOINED.
DR      EMBL, AF391187; AAL40929.1; JOINED.
DR      EMBL, AF391188; AAL40929.1; JOINED.
DR      EMBL, AF391189; AAL40929.1; JOINED.
DR      EMBL, BC003989; AAL03989.1; -.
DR      HSSP; Q9Y297; IP22.
DR      MGD; MGI:133871; Btrc.
DR      GO; GO:0016874; F-ligase activity; IEA.
DR      InterPro; IPR001810; F-box.
DR      InterPro; IPR01680; WD40.
DR      InterPro; IPR01046; WD40-like.
DR      Pfam; PF00646; F-box; 1.
DR      Pfam; PF00400; WD40; 7.

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DR PRINTS: PR00320: GPROTEINBRPT.
DR Prodom: PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KM Ligase; Repeat; WD repeat.
SQ SEQUENCE 569 AA; 65105 MW; BC7D6544815B2296 CRC64;

Query Match          98.8%; Score 2997; DB 2; Length 569;
Best Local Similarity 98.6%; Pred. No. 5,1e-217;
Matches 561; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFNMSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNDETVCIA 60
DB 1 MDPAAVLQEKALKFNMSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNDETVCIL 60
QY 61 STAKTENCVAKKTLANGTSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFEVHL 120
DB 61 STAKTENCVAKKTLANGTSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFEVHL 120
QY 121 ISQCHYOHGHINSYLPMLQRPDFTALPARGLDHIENILSYLDAKSLCAAEIVCKEMY 180
DB 121 ISQCHYOHGHINSYLPMLQRPDFTALPARGLDHIENILSYLDAKSLCAAEIVCKEMY 180
QY 181 RVTSDGMLMKKLIERRVRTSLMRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
DB 181 RVTSDGMLMKKLIERRVRTSLMRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
QY 241 ODITETSNMRCGHSIORHCRSETSKGYVCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
DB 241 ODITETSNMRCGHSIORHCRSETSKGYVCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
QY 301 RILGHTGSVLCLOYDERVIIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360
DB 301 RILGHTGSVLCLOYDERVIIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360
QY 361 VTGSKDRSIAVWMASTPDTITLRVLVGHRAAVNVVDFDKYIVSAGDRITIKWNTSTC 420
DB 361 VTGSKDRSIAVWMASTPDTITLRVLVGHRAAVNVVDFDKYIVSAGDRITIKWNTSTC 420
QY 421 EFVRTLNGHKRGIACTQYRDLVVGSSDNTIRLMDIECGACRLVLEGHEELVRCIRPDN 480
DB 421 EFVRTLNGHKRGIACTQYRDLVVGSSDNTIRLMDIECGACRLVLEGHEELVRCIRPDN 480
QY 481 KRIVSAYDGKIKWDLVAALDPAPAGTLCRLTVHSGRVFRLQDFEFOIVSSSHDT 540
DB 481 KRIVSAYDGKIKWDLVAALDPAPAGTLCRLTVHSGRVFRLQDFEFOIVSSSHDT 540
QY 541 ILIWDPLNDPAQAEPSPSPRTYIISR 569
DB 541 ILIWDPLNDPAQAEPSPSPRTYIISR 569

RESULT 3
ID Q92159 PRELIMINARY; PRT; 569 AA.
AC Q92159;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE Beta-creneducin repeat containing protein.
OS Name=Btcr;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99145465; PubMed=9990853;
RA Spencer E., Jiang J., Chen Z.J.;
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RT "Signal-induced ubiquitination of IkappaBalpha by the F-box protein
RT RT s1mb/beta-Trcp ";
RL Genes Dev. 13:284-294(1999).
CC -1- Similarity: Contains 7 WD repeats.
DR EMBL; AF112979; AAD04181.1; -.
DR HSSP; Q9Y297; 1P22.
DR MGD; MGI:1338871; Btcr.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_Like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR Prodom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KM Repeat; WD repeat.
SQ SEQUENCE 569 AA; 65047 MW; BC7C7A44815BED96 CRC64;

Query Match          98.5%; Score 2990; DB 2; Length 569;
Best Local Similarity 98.4%; Pred. No. 1,7e-216;
Matches 560; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDPAAVLQEKALKFNMSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNDETVCIA 60
DB 1 MDPAAVLQEKALKFNMSEREDCNNGEPKRIIPKNSLRQTYNSCARLCLNDETVCIL 60
QY 61 STAKTENCVAKKTLANGTSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFEVHL 120
DB 61 STAKTENCVAKKTLANGTSMIVPKORKLSASYEKEKELCVKFEQMSSEDOVEFEVHL 120
QY 121 ISQCHYOHGHINSYLPMLQRPDFTALPARGLDHIENILSYLDAKSLCAAEIVCKEMY 180
DB 121 ISQCHYOHGHINSYLPMLQRPDFTALPARGLDHIENILSYLDAKSLCAAEIVCKEMY 180
QY 181 RVTSDGMLMKKLIERRVRTSLMRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
DB 181 RVTSDGMLMKKLIERRVRTSLMRGLAERRGQGYLFKNKPPDGNAPNSFYRALYPKII 240
QY 241 ODITETSNMRCGHSIORHCRSETSKGYVCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
DB 241 ODITETSNMRCGHSIORHCRSETSKGYVCLQYDDQKIVSGLRDNTIKIMDKNTLECK 300
QY 301 RILGHTGSVLCLOYDERVIIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360
DB 301 RILGHTGSVLCLOYDERVIIITGSSDSTVRWVDVNTGEMLNTLIHCEAVLHLRFNNGM 360
QY 361 VTGSKDRSIAVWMASTPDTITLRVLVGHRAAVNVVDFDKYIVSAGDRITIKWNTSTC 420
DB 361 VTGSKDRSIAVWMASTPDTITLRVLVGHRAAVNVVDFDKYIVSAGDRITIKWNTSTC 420
QY 421 EFVRTLNGHKRGIACTQYRDLVVGSSDNTIRLMDIECGACRLVLEGHEELVRCIRPDN 480
DB 421 EFVRTLNGHKRGIACTQYRDLVVGSSDNTIRLMDIECGACRLVLEGHEELVRCIRPDN 480
QY 481 KRIVSAYDGKIKWDLVAALDPAPAGTLCRLTVHSGRVFRLQDFEFOIVSSSHDT 540
DB 481 KRIVSAYDGKIKWDLVAALDPAPAGTLCRLTVHSGRVFRLQDFEFOIVSSSHDT 540
QY 541 ILIWDPLNDPAQAEPSPSPRTYIISR 569
DB 541 ILIWDPLNDPAQAEPSPSPRTYIISR 569

RESULT 4
ID Q9R1G7 PRELIMINARY; PRT; 569 AA.
AC Q9R1G7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
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DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DR Beta-transducin repeat-containing protein.
GN Name=Btrc;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Winston J., Elledge S.J., Harper J.W.;
RC Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 7 WD repeats.
DR EMBL; AF10396; AAD41025.1; -.
DR HSSP; Q9Y297; 1P22.
DR MGD; MGI:1338871; Btrc.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_1like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS00682; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 569 AA; 65209 MW; E6DDCAD28D551D9D CRC64;

Query Match 98.2%; Score 2978; DB 2; Length 569;
Best Local Similarity 97.9%; Pred. No. 1.4e-215;

Matches 557; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDPAAVLOEKALKFNSSEREDCNNGEPKRIIPKNSLRQTVNSCARLCINQETVCL 60
DB 1 MDPAAVLOEKALKFNSSEREDCNNGEPKRIIPKNSLRQTVNSCARLCINQETVCL 60
QY 61 STAMKTEHCVAATKLANGTSSMIVPRQKLSASYEKEKELCVYFQWESQDVEFEHL 120
DB 61 STAMKTEHCVAATKLANGTSSMIVPRQKLSASYEKEKELCVYFQWESQDVEFEHL 120
QY 121 ISOMCHYQGHINSYIKPMLQDFTALPARGLDHTAENILSYLDAKSCAAELVCKEY 180
DB 121 ISOMCHYQGHINSYIKPMLQDFTALPARGLDHTAENILSYLDAKSCAAELVCKEY 180
QY 121 ISOMCHYQGHINSYIKPMLQDFTALPARGLDHTAENILSYLDAKSCAAELVCKEY 180
DB 121 ISOMCHYQGHINSYIKPMLQDFTALPARGLDHTAENILSYLDAKSCAAELVCKEY 180
QY 181 RYTSQDMLMKKLIERNVRTDSLWRGLAERBGQYLFKPKPPGNAPRNSFYRALYPKII 240
DB 181 RYTSQDMLMKKLIERNVRTDSLWRGLAERBGQYLFKPKPPGNAPRNSFYRALYPKII 240
QY 181 RYTSQDMLMKKLIERNVRTDSLWRGLAERBGQYLFKPKPPGNAPRNSFYRALYPKII 240
DB 181 RYTSQDMLMKKLIERNVRTDSLWRGLAERBGQYLFKPKPPGNAPRNSFYRALYPKII 240
QY 241 QDIETIESNMRGSRHSIORHCRSETSKGVYCLQYDQKIVSGLRDNITIKIWDKNTLECK 300
DB 241 QDIETIESNMRGSRHSIORHCRSETSKGVYCLQYDQKIVSGLRDNITIKIWDKNTLECK 300
QY 241 QDIETIESNMRGSRHSIORHCRSETSKGVYCLQYDQKIVSGLRDNITIKIWDKNTLECK 300
DB 241 QDIETIESNMRGSRHSIORHCRSETSKGVYCLQYDQKIVSGLRDNITIKIWDKNTLECK 300
QY 301 RILTGHTGSQLQYDERVIITGSSSDSYRWDVNTGEMNLTIHHCEAVLHFRNNGM 360
DB 301 RILTGHTGSQLQYDERVIITGSSSDSYRWDVNTGEMNLTIHHCEAVLHFRNNGM 360
QY 301 RILTGHTGSQLQYDERVIITGSSSDSYRWDVNTGEMNLTIHHCEAVLHFRNNGM 360
DB 301 RILTGHTGSQLQYDERVIITGSSSDSYRWDVNTGEMNLTIHHCEAVLHFRNNGM 360
QY 361 VTCSKDRSIADVMDSPDTITLRRVYVGRRAAVNVDPDKYIVASAGRTIKWNTSTC 420
DB 361 VTCSKDRSIADVMDSPDTITLRRVYVGRRAAVNVDPDKYIVASAGRTIKWNTSTC 420
QY 361 VTCSKDRSIADVMDSPDTITLRRVYVGRRAAVNVDPDKYIVASAGRTIKWNTSTC 420
DB 361 VTCSKDRSIADVMDSPDTITLRRVYVGRRAAVNVDPDKYIVASAGRTIKWNTSTC 420
QY 421 EFVRLTLNGHKGSIACIQYDRDLVSSGSSDNTIRLMDIEGACILVLEGHEELVRCIRFDN 480
DB 421 EFVRLTLNGHKGSIACIQYDRDLVSSGSSDNTIRLMDIEGACILVLEGHEELVRCIRFDN 480
QY 421 EFVRLTLNGHKGSIACIQYDRDLVSSGSSDNTIRLMDIEGACILVLEGHEELVRCIRFDN 480
DB 421 EFVRLTLNGHKGSIACIQYDRDLVSSGSSDNTIRLMDIEGACILVLEGHEELVRCIRFDN 480
QY 481 KRIIVGAVYGGKIKWMDLVAAALDPRAAGTLCRTLVEHSGRFRLODFEQIVSSSHDT 540
DB 481 KRIIVGAVYGGKIKWMDLVAAALDPRAAGTLCRTLVEHSGRFRLODFEQIVSSSHDT 540
QY 481 KRIIVGAVYGGKIKWMDLVAAALDPRAAGTLCRTLVEHSGRFRLODFEQIVSSSHDT 540
DB 481 KRIIVGAVYGGKIKWMDLVAAALDPRAAGTLCRTLVEHSGRFRLODFEQIVSSSHDT 540
QY 541 ILIWDPLNDPAQAEPSPRSRTYTYISR 569

DB 541 ILIWDPLNDPAQAEPSPRSRTYTYISR 569

RESULT 5
Q68DSO PRELIMINARY; PRT; 564 AA.
ID 068DSO;
AC 068DSO;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DE Hypothetical protein DKFZp781N011.
GN Name=DKFZp781N011.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=amygdala;
RG The German cDNA Consortium;
RA Koerner K., Beyer A., Mewes H.W., Weil B., Amid C., Oanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 7 WD repeats.
DR EMBL; CR749295; CAH18150.1; -.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_1like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINBRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS00682; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 564 AA; 64201 MW; 5CCF0A7C5A59B5C1 CRC64;

Query Match 93.0%; Score 2821; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 8.9e-204;

Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 QTVNSCARLCINQETVCLASTAMKTEHCVAATKLANGTSSMIVPRQKLSASYEKEKELC 101
DB 37 QTVNSCARLCINQETVCLASTAMKTEHCVAATKLANGTSSMIVPRQKLSASYEKEKELC 96
QY 102 VKYFQWESQDVEFEHLISOMCHYQGHINSYIKPMLQDFTALPARGLDHTAENIL 161
DB 97 VKYFQWESQDVEFEHLISOMCHYQGHINSYIKPMLQDFTALPARGLDHTAENIL 156
QY 162 SYLDAKSCAAELVCKEYRVTSDGLMKKLIERNVRTDSLWRGLAERBGQYLFKPKPP 221
DB 157 SYLDAKSCAAELVCKEYRVTSDGLMKKLIERNVRTDSLWRGLAERBGQYLFKPKPP 216
QY 222 PDGNAPRNSFYRALYPKIIQDIETIESNMRGSRHSIORHCRSETSKGVYCLQYDQKIV 281
DB 217 PDGNAPRNSFYRALYPKIIQDIETIESNMRGSRHSIORHCRSETSKGVYCLQYDQKIV 276
QY 277 SGLRDNITIKIWDKNTLECKRIITGHTGSQLQYDERVIITGSSSDSYRWDVNTGEMNL 341
DB 282 SGLRDNITIKIWDKNTLECKRIITGHTGSQLQYDERVIITGSSSDSYRWDVNTGEMNL 341
QY 342 TLIIHCEAVLHFRNNGMVTCSKDRSIADVMDSPDTITLRRVYVGRRAAVNVDPDK 401
DB 337 TLIIHCEAVLHFRNNGMVTCSKDRSIADVMDSPDTITLRRVYVGRRAAVNVDPDK 396
QY 402 YIVSASGRTIKWNTSTCEFRVTLNGHKGSIACIQYDRDLVSSGSSDNTIRLMDIEGCA 461
DB 397 YIVSASGRTIKWNTSTCEFRVTLNGHKGSIACIQYDRDLVSSGSSDNTIRLMDIEGCA 456

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QY 462 CLRVLGHEELVRCIRFPNKRIVSGAYDGKIYVWMLVAALDPRAPAGTLCLRTIVESHGR 521
DB 457 CLRVLGHEELVRCIRFPNKRIVSGAYDGKIYVWMLVAALDPRAPAGTLCLRTIVESHGR 516
QY 522 VFRLOPDEFQIVSSSHDITLIMDELNDPAQAEPSPRSRTIYISR 569
DB 517 VFRLOPDEFQIVSSSHDITLIMDELNDPAQAEPSPRSRTIYISR 564

RESULT 6
ID TRCB_XENLA STANDARD: PRT: 518 AA.
AC 091854: P70037; P70038;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Beta-T-CP (Beta-transducin repeat-containing protein).
GN Name=FBXW1; Synonyms=BTRCP;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RX MEDLINE=93330289; PubMed=8393141;
RA Spevak W., Keiper B.D., Stratowa C., Castranon M.J.;
RT "Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
RT anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein with
RT beta-transducin repeats."
RL Mol. Cell. Biol. 13:4953-4966(1993).
RP [2]
RX MEDLINE=97109804; PubMed=8952061;
RX DOI=10.1002/(SICI)1520-6408(1996)19:3<190::AID-DVG2>3.3.CO;2-Y;
RA Hudson J.W., Alarcon V.B., Elinson R.P.;
RT "Identification of new localized RNAs in the Xenopus oocyte by
RT differential display PCR."
RL Dev. Genet. 19:190-198(1996).
CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
CC proteins and promotes their ubiquitination and degradation. May
CC participate in Wnt signaling.
CC -1- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
CC (by similarity).
CC -1- DEVELOPMENTAL STAGE: Present in fully grown and progesterone-
CC matured oocytes. The level change very little even after zygotic
CC gene transcription begins following the midblastula transition. Do
CC not increase in abundance in the gastrula, neurula, tailbud, or
CC tadpole embryo.
CC -1- SIMILARITY: Contains 1 F-box domain.
CC -1- SIMILARITY: Contains 7 WD repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M98268; AAA02810.1; -
DR EMBL: U63921; AAB49671.1; -
DR EMBL: U63922; AAB49672.1; -
DR PIR: B48088; B48088.
DR HSSP: Q9Y297; I222.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR008945; Skp1_Skp2.
DR InterPro: IPR001680; WD40_
DR InterPro: IPR01046; WD40_like.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.

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DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 1.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 6.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD1 conjugation pathway; WD repeat; Wnt signaling pathway.
FT DOMAIN 119 157 F-box.
FT REPEAT 230 258 WD 1.
FT REPEAT 270 298 WD 2.
FT REPEAT 310 338 WD 3.
FT REPEAT 353 381 WD 4.
FT REPEAT 393 421 WD 5.
FT REPEAT 433 461 WD 6.
FT REPEAT 482 510 WD 7.
FT CONFLICT 302 304 GEM -> EFR (in Ref. 2).
FT CONFLICT 516 518 GLA -> AAH (in Ref. 2).
SQ SEQUENCE 518 AA; 59507 MW; 2A52EC19028127E3 CRC64;

Query Match 85.6%; Score 2597; DB 1; Length 518;
Best Local Similarity 91.6%; Pred. No. 5.8e-187;
Matches 488; Conservative 7; Mismatches 8; Indels 30; Gaps 1;

QY 18 SSEREDCNNGEPKRIIPKNSLRQYNSCARCLCNOETVCLASTAMKTENCVAKTILAN 77
DB 13 ASEREDCNRPBPRIITENTILRO-----TILAN 42
QY 78 GTSSMIVPKRKLSASYEKEKELCVKYFEOWSESQVEFVHLLISQCHYOHGINSYLYK 137
DB 43 GTSSMIVPKRKLSANYEKEKELCVKYFEQWSECQVEFVHLLISRMCHYOHGINSYLYK 102
QY 138 PMLQRFDTALPARGLHIANLILSYDAKSLCAELVCKEWYVTSDDGMKLLIRMV 197
DB 103 PMLQRFDTALPARGLHIANLILSYDAKSLCAELVCKEWYVTSDDGMKLLIRMV 162
QY 198 RTDSLWGLAERRRGQYLFPNKRPPDGNAPNSFYRALPYKLIQDIETISNMRGHRSL 257
DB 163 RTDSLWGLAERRRGQYLFNKRPPDGTPTNSFYRALPYKLIQDIETISNMRGHRSL 222
QY 258 QRIHCRSETSGKVCLQYDDQKIVSGLRDNTIKIWDKNLYECKILTGHGTSVLCLOYDE 317
DB 223 QRIHCRSETSGKVCLQYDDQKIVSGLRDNTIKIWDKNLYECKILTGHGTSVLCLOYDE 282
QY 318 RVITTSQSDSVRWVDVNTGEMLNTLIHRCAGVLAHLFPNNGMVTCSKDRSIAVDMASA 377
DB 283 RVITTSQSDSVRWVDVNTGEMLNTLIHRCAGVLAHLFPNNGMVTCSKDRSIAVDMASA 342
QY 378 TDITLRRLVGHRAAVNVVDPDDKIVSASGDRITIKYWNSTSCFVFTLNGHKGIACTQ 437
DB 343 TDITLRRLVGHRAAVNVVDPDDKIVSASGDRITIKYWNSTSCFVFTLNGHKGIACTQ 402
QY 438 YRDLVVGSSDNTIRLMDIEGACLVLBGHEELVRCIRFPNKRIVSGAYDGKIKWDL 497
DB 403 YRDLVVGSSDNTIRLMDIEGACLVLBGHEELVRCIRFPNKRIVSGAYDGKIKWDL 462
QY 498 VVALDPRAPAGTLCRLTVESHGVRFLQPEQIVSSSHDITLIMDELNDP 550
DB 463 VVALDPRAPAGTLCRLTVESHGVRFLQPEQIVSSSHDITLIMDELNDP 515

RESULT 7
QY 08BY90 PRELIMINARY; PRT: 529 AA.
AC 08BY90;
DT 01-MAR-2003 (TRENBLREL. 23, Created)
DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA. RIKEN full-length enriched
DE library, clone: A630019L11 product: F-box/WD-REPEAT PROTEIN 1B (F-BOX
DE AND WD-REPEATS PROTEIN BETA-TRCP2) homolog.
GN Name=Fbxw1; Synonyms=Fbxw1b;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganari Y., Shibata K., Itoh M.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsunai T., Taahiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system: 384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K.,

DR	ProDom; P0000018; WD40; 4.
DR	SMART; SM00256; FBOX; 1.
DR	SMART; SM00320; WD40; 7.
DR	PROSITE; PS50181; FBOX; 1.
DR	PROSITE; PS00678; WD_REPEATS_1; 5.
DR	PROSITE; PS50082; WD_REPEATS_2; 7.
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW	Repeat; WD repeat.
SQ	SEQUENCE 529 AA; 60812 MW; D2F382457FD80080 CRC64;

Query Match	78.9%; Score 2395; DB 2; Length 529;
Best Local Similarity	78.9%; Pred.No. 9.7e-172;
Matches 449; Conservative	43; Mismatches 37; Indels 40; Gaps 3;

OY	1	MDPAEAVLQEKALVFNNSSEREDCNNEBPRIKIPENKSLRQTYNSCARLCINQETVCLA	60
Db	1	MEP-DSTVEIKTTEILMNTSVMEODNEBSPRK-----	31
OY	61	STAMKTENCVAKTKLANGTSMTVPKORKLSASYEKEKELCVKYFEOWSSDOYEVEHL	120
Db	32	-----SALMQISNGTSVSIVSRKRPEBGNYQKEKDCLIKFPDQMSSDOYEFVEHL	82
OY	121	ISOMCHVOHGINSYLPMLOPDDITLTPARGDHILENLSYLDASLCAAEIYCWEY	180
Db	83	ISRRCQHGHGINSYLPMLQRDPDTLPPQGDHIAENILSYLDASLCAAEIYCWEQ	142
OY	181	RVTSDGMLEMKLLIRMYRTDSLMEGLERBGWGCGYLFKNRPDGNAFPNSFYRLPKII	240
Db	143	RVISGMLMKLLIRMYRTDPLMKGLSERKGMDGYLFKNRPTDS--PNNSFYRLPKII	200
OY	241	QDIETIESNRCCGHSIORIHCRSETSKGYVCLQYDDOKIVSGLRDNTIKIMDKNTLECK	300
Db	201	QDIETIESNRCCGHRNLORIQCRENSKGYVCLQYDDDKLIISGLRDNSIKIMDKSIECL	260
OY	301	RILFTGHGSVLCLOYDERVIITGSSDSSTVAVVMVDYNGEMANTLIHQEEAVALHLPFNNGM	360
Db	261	KVLIGHGHSVLCLOYDERVIITGSSDSSTVAVMVNDGEVINTLIHNHEAVALHLPFSGLM	320
OY	361	VTCSDKRSIAWMVASPTDITLRLVVLGHBAVANVDPDDRYIVSAGSDRTIKVMNSTC	420
Db	321	VTCSDKRSIAWMVASATDITLRLVVLGHBAVANVDFDKYIVSAGSDRTIKWMSITC	380
OY	421	EPVATTINGHKRGIACTLOYDRLVVSGSSDNTIRLMIDEGACULVLEGHELVRCLRFDN	480
Db	381	EPVATTINGHKRGIACTLOYDRLVVSGSSDNTIRLMIDEGACULVLEGHELVRCLRIFDN	440
OY	481	KRIYSAGYDGKIKYKWDIVAAIDPRAPAGTYCLRTLVESHGRVFRLOPFDEFOIYSSSHDT	540
Db	441	KRIYSAGYDGIKIKWIDLQAALDPRAPASTLCRLTLVESHGRVFRLOPFDEFOIYSSSHDT	500
OY	541	ILIMDFLNPDAQAQEPSPRSRYTYYSR	569
Db	501	ILIMDFLNPVPSAQONETRSPSRITYTYSR	529

RESULT 8			
ID	FW1B_HUMAN	STANDARD;	PRT; 542 AA.
AC	O9UKX1; O9PZ88; O9PZS9; O9Y4G6;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, last annotation update)		
DE	F-box/WD-repeat protein 11 (F-box/WD-repeat protein 1B) (F-box and WD-		
DE	repeats protein beta-TTCP2).		
GN	Name=FBXW11; Synonym=s-BTRCP2; FW1B; FBXW1B; KIAA0696;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;		
DX	Cenciarelli C., Chaitau D.S., Guardavaccaro D., Parks W., Vidal M.		

RA Pagano M.;
 RT "Identification of a family of human F-box proteins.";
 RL Curr. Biol. 9:1177-1179(1999).
 RN [2]
 RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RP TISSUE=Fetal lung;
 RC MEDLINE=20160458; PubMed=10694485; DOI=10.1006/birc.2000.2241;
 RX Kojke J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
 RA Katch M.;
 RT "Molecular cloning and genomic structure of the betarTRCP2 gene on
 RT chromosome 5q35.1.";
 RL Biochem. Biophys. Res. Commun. 269:103-109(2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=98403880; PubMed=9734811;
 RX Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM B).
 RP TISSUE=Lymph;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klansner R.D., Collins S.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefter C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Cantucci P., Prange C.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.D., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Probably recognizes and binds to some phosphorylated
 CC proteins and promotes their ubiquitination and degradation. May
 CC participate in Wnt signaling.
 CC -1- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=C;
 CC IsoId=G9UKB1-1; Sequence=Displayed;
 CC Name=A;
 CC IsoId=G9UKB1-2; Sequence=VSP_006765;
 CC Name=B;
 CC IsoId=G9UKB1-3; Sequence=VSP_006766;
 CC -1- SIMILARITY: Contains 1 F-box domain.
 CC -1- SIMILARITY: Contains 7 WD repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, AF176022; AAF04528.1; -;
 CC DR EMBL, AB033279; BAA92329.1; -;
 CC DR EMBL, AB033280; BAA92330.1; -;

DR EMBL, AB033281; BAA92331.1; -; ALT_INTR.
 DR EMBL, AB014596; BAA31671.1; -;
 DR EMBL, BC026213; AAH26213.1; -;
 DR HSSP, Q91297; IIP22.
 DR InLAc; Q9UKB1; -;
 DR GeneW; HGNC:13607; FBXW11.
 DR H-InVDB; HIX0005413; -;
 DR MIM; 605651; -;
 DR GO; GO:0000151; C:ubiquitin ligase complex; NAS.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; NAS.
 DR GO; GO:0016567; P:protein ubiquitination; NAS.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR008945; SKP1 Skp2.
 DR InterPro; IPR001680; WD40-
 DR InterPro; IPR011046; WD40_like.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR ProDom; PD000018; WD40; 4.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS50082; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 DR KX Alternative splicing; Repeat; ubl conjugation pathway; WD repeat;
 DR KX Wnt signaling pathway.
 DR DOMAIN 129 167 F-box.
 FT REPEAT 238 275 WD 1.
 FT REPEAT 278 315 WD 2.
 FT REPEAT 318 355 WD 3.
 FT REPEAT 361 398 WD 4.
 FT REPEAT 401 440 WD 5.
 FT REPEAT 442 478 WD 6.
 FT REPEAT 490 527 WD 7.
 FT VARSPLIC 16 49 Missing (in isoform A).
 FT VARSPLIC 16 48 /Frid=VSP_006765.
 FT VARSPLIC 16 48 CSVPRLSLGICANLVESMCALSCIQSMPSVRL -> NTSV
 FT MEDQNDSPKRTLW (in isoform B).
 FT /Frid=VSP_006766.
 SQ SEQUENCE 542 AA; 62090 MM; 7CD4087EFAA5C8A CRC64;
 Query Match 78.6%; Score 2384.5; DB 1; Length 542;
 Best Local Similarity 79.0%; Pred. No. 6.2e-171;
 Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;
 QY 1 MDPAAVLOEKALFENMSEREDCNNGEPPRKIKPKNSLRQTNSCARLCLNQETCIA 60
 DB 1 MEP-DSVIEDKTIELMCS-----VP-----RSLWGCANLV--ESMCAL 36
 QY 61 S--TAMKTENCVAKTKLANGTSSMIVPQRKLSASYEKELCVKFEOMSESQOVEFE 118
 DB 37 SCLQSMPSVRL---QISNGTSSVIVSRKRPSSEGNQKXNDLCIKYFDQMSQOVEFE 93
 QY 119 HLISQMGCHYOHGHINSYLYKPMLOQDFITLALPARGLDHIHENIISYLDAKSICAEVYCKE 178
 DB 94 HLISRMCHYOHGHINSYLYKPMLOQDFITLALPEQGLDHIHENIISYLDARSICAEVYCKE 153
 QY 179 MYRTSGMLMKKILIEBMYRTDSLMRGLAERRGGOYLFPKRPDGNAPPSFYRALYPK 238
 DB 154 WQVYSBGMMLKKLIERVVRDPLMKGLSEERGMDOYLFKRPDQ--PPVSFTRSLYPK 211
 QY 239 IIODIETTESNMRGSRSLORIHCRSETSKGVYCLQVDDQKIVSGLRDNTIKIWDKNTLE 298
 DB 212 IIODIETTESNMRGSRNLQRIOGRSNSKGVYCLQVDDKILISGLDNSIKIKDKTSLE 271
 QY 299 CKRILTGHTGSVLCLODERVITIGSSDSYRVVDVNTGEMANTLIHCEAVLHLPKNG 358
 DB 272 CLKVLTGHTGSVLCLODERVITIGSSDSYRVVDVNTGELVANTLIHNEAVLHLPKNSG 331
 QY 359 MMVTCSDKRSIAVWDMASPDITLRYLVNGRAVNVVDPDDKIVSASGRTIKWNTS 418
 DB 332 LMVTCSDKRSIAVWDMASDITLRYLVNGRAVNVVDPDDKIVSASGRTIKWNTS 391
 QY 419 TCFEVRTLNGHKGRIACIQYRDLRVSGSSDNTIRLMDIECGACLRVLEGEHELVRCTIRF 478


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DB 392 TCEPRTLNHGRGIACIQYRDLVYSSSDNTIRIMDEICACLRVLGHEHETVRCIRF 451
QY 479 DNKRIVSGAYDGKIKYWDVVAIDPAPAGTCLRTLVHSGRVFLQGFDEFOIYSSSHD 538
DB 452 DNKRIVSGAYDGKIKYWDVVAIDPAPAGTCLRTLVHSGRVFLQGFDEFOIYSSSHD 511
QY 539 DTLLIMDFLNDPAPAGAEPPSPRTTYISR 569
DB 512 DTLLIMDFLNDPAPAGAEPPSPRTTYISR 542

RESULT 9
08K022 PRELIMINARY; PRT; 563 AA.
AC 08K022;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE F-box and WD-40 domain protein 11.
GN Name=Fbxw11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheinen C.M., Schler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
RA Villalón D.K., Muzny K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maier M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
CC -1- SIMILARITY: Contains 7 WD repeats.
DR EMBL: BC034261; AAK34261.1; -.
DR HSSP: Q9Y297; 1P22.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR InterPro: IPR011046; WD40_like.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.
DR ProDom: PD000018; WD40; 4.
DR SMART: SM00256; FBOX; 1.
DR SMART: SM00320; WD40; 7.
DR PROSITE: PSS0181; FBOX; 1.
DR PROSITE: PSS0678; WD_REPEATS_1; 5.
DR PROSITE: PSS0082; WD_REPEATS_2; 7.
DR PROSITE: PSS0294; WD_REPEATS_REGION; 1.
DR Repeat; WD repeat.
KW Repeat; WD repeat.
SQ SEQUENCE 563 AA; 64481 MW; 74D07E6B850ABED CRC64;

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Query Match 78.4%; Score 2380; DB 2; Length 563;
Best Local Similarity 78.1%; Pred. No. 1.4e-170;
Matches 454; Conservative 46; Mismatches 51; Indels 30; Gaps 7;

QY 1 MDPAAVLQEKALKFENSSERE---DNNGBPPRKIIPEKNSLRQYNSCARCLNQ--E 55
DB 1 MEP-DSVIEDKTIELMCSVPRSLWGCAN-----LVESNCALSLQGSMS 44
QY 56 TVCLASTA-MKTEN-----CVAKTKLANGTSSMTVPKORKLSAYEKELCVKFFEW 108
DB 45 VACLQNTSVEMQDNDDESPKRSALWQISNGTSVIVSRPSPBEGYQKQKDCIKYFDWM 104
QY 109 SESDQVEFVEHLISOMCYOHGHINSYLPKMQRPFITLPAARGDHIENILSYIDAKS 168
DB 105 SESDQVEFVEHLISOMCYOHGHINSYLPKMQRPFITLPAARGDHIENILSYIDAKS 164
QY 169 LCAAEVLVCKEYRYVTSQGLMVKGLIERVYRTDLSLRGLAERRGQYLFKNKPPGNAP 228
DB 165 LCAAEVLVCKEYRYVTSQGLMVKGLIERVYRTDLSLRGLAERRGQYLFKNKPPGNAP 222
QY 229 NSFYRALPKTIQDIETIESNWRCCRHSIORHCHSEFSKGYCYQYDDKTIISGLRDT 288
DB 223 NSFYSLVPKTIQDIETIESNWRCCRHNIOIQCRSENSKGYCYQYDDKTIISGLRDS 282
QY 289 IKIMDKNTLECKRILTGHGTVLCTQYDERVITGSSDSQTVRVMVDGEMTLIHICE 348
DB 283 IKIMDKSLECKLVLTGHGTVLCTQYDERVITGSSDSQTVRVMVDGEMTLIHINE 342
QY 349 AVTLHLRFNNGMVNTCSKORSIAVWDMASPTDITLRLVYVGHRAAVNVVDFDDKYIVSASG 408
DB 343 AVTLHLRFNSGLMNTCSKORSIAVWDMASPTDITLRLVYVGHRAAVNVVDFDDKYIVSASG 402
QY 409 DRTIVYNTSTEEFRTLNHGRGIACIQYRDLVYSSSDNTIRIMDEICACLRVLG 468
DB 403 DRTIVYNTSTEEFRTLNHGRGIACIQYRDLVYSSSDNTIRIMDEICACLRVLG 462
QY 469 HEELVRCRFPDKRIVSGAYDGKIKYWDVVAIDPAPAGTCLRTLVHSGRVFLQGF 528
DB 463 HEELVRCRFPDKRIVSGAYDGKIKYWDVVAIDPAPAGTCLRTLVHSGRVFLQGF 522
QY 529 EFQIVSSSHDDTLLIMDFLNDPAPAGAEPPSPRTTYISR 569
DB 523 EFQIVSSSHDDTLLIMDFLNDPAPAGAEPPSPRTTYISR 563

RESULT 10
08CHDS PRELIMINARY; PRT; 555 AA.
AC 08CHDS;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MKIAA0696 protein (Fragment).
GN Name=Fpxw11; Synonym=Fpxw1b, MKIAA0696;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RX Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 7 WD repeats.
DR EMBL: AB093260; BACA1444.1; -.
DR HSSP: Q9Y297; 1P22.
DR MGD: MGI:2144023; Fpxw11.
DR InterPro: IPR001810; F-box.
DR InterPro: IPR001680; WD40.
DR InterPro: IPR011046; WD40_like.
DR Pfam: PF00646; F-box; 1.
DR Pfam: PF00400; WD40; 7.

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DR PRINTS; PR00320; GPROTEINERTPT.
DR PR0Dom; PD000018; WD40; 4.
DR SMART; SM00256; FB0X; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS50181; FB0X; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
FT NON_TER 1 1
SQ SEQUENCE 555 AA; 63287 MW; 6025496DBAC6A489 CRC64;

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DT 05-JUL-2004 (TReMBLrel. 27, last annotation update)
 DE Zgc:63728.
 GN ORFNames=zgc:63728;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maier M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX Strausberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 CC -i- SIMILARITY: Contains 7 WD repeats.
 DR EMBL, BC056809; AAH56809.1; -
 DR ZFIN, ZDB-GENE-040426-2303; zgc:63728.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR01680; WD40.
 DR InterPro; IPR01046; WD40_like.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR ProDom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PSS0181; FBOX; 1.
 DR PROSITE; PSS00678; WD_REPEATS_1; 5.
 DR PROSITE; PSS0082; WD_REPEATS_2; 7.
 DR PROSITE; PSS0294; WD_REPEATS_REGION; 1.
 DR Repeat; WD repeat.
 SQ SEQUENCE 527 AA; 60546 MW; 563F3C014CA099C3 CRC64;
 Query Match 74.4%; Score 2258.5; DB 2; Length 527;
 Best Local Similarity 76.1%; Pred. No. 1.8e-161;
 Matches 430; Conservative 49; Mismatches 45; Indels 41; Gaps 6;
 QY 8 LQKLLKFNSSEREDCNNGEPKRIPEKSLRQTVNSCARLQNGEN-VCLASAMKT 66
 DB 1 MEDKTLQGNISVMD-----QIADNSPKITLIKSTFTIC----- 34
 QY 67 ENCAVKTKLANG--TSSMIVPKORKLSAYEKEKEKLCVYFPMOWSSDVEFEVHLISQM 124
 DB 35 -----PQVSNGLPLGSS-----KKRPSEGNYEKEKDVCIQLFQWGSADQVEFEVHLISM 84
 QY 125 CHYOHGHTNSYLKPMLOGRFITALPARGLDHIAENLITLIDAKSLCAALVCKEKWRVTS 184
 DB 85 CHYOHGHTNSYLKPMLOGRFITALPARGLDHIAENLITLIDAKSLCAALVCKEKWRVTS 144
 QY 185 DQMLWKILERMVVRTDLSLRGLAERGMQVLFKNKPPDGNAPPNSSFYALPKTIQDIE 244

DB 145 EGMWKKILERMVVRTDPLMKGLSERHQMEKYLFRKRTTE--VPPNSYNSLVPKIIQDIE 202
 QY 245 TIESNWRGCRNALQRIHCRSETSKGYVLCIQYDQDKIVSLRNTTIKIMKNTLECKRIIT 304
 DB 203 TIEANWRCGRNHLQRIQCSSEKSGYVLCIQYDEKXISGLRDNISIKIMDKQTECLKIIT 262
 QY 305 GHTGSVLCIQYERVIITGSSSDSTVRVMDVNTGEMLNTLIHHCEAVLHLRFNNGMVTS 364
 DB 263 GHTGSVLCIQYERVIITGSSSDSTVRVMDVNSGVALNTLIHNEAVLHLRFNGLAVTOS 322
 QY 365 KDRSLAVMDMASPTITLRLRVLVGRRAAVNVVDFDKIVSASGRTIKVMNTSCEFYR 424
 DB 323 KDRSLAVMDMASPTITLRLRVLVGRRAAVNVVDFDKIVSASGRTIKVMNTSCEFYR 382
 QY 425 TLNGHKGRIACIQYDRILVSSGSSDNTIRLMDIEGACILRVIEGHELVRCIRPDNKRIV 484
 DB 383 TLNGHKGRIACIQYDRILVSSGSSDNTIRLMDIEGACILRVIEGHELVRCIRPDNKRIV 442
 QY 485 SGAYNGKIKVMDLVAALDPRAAGTLCRTVYHSGRVPRLOPDEFQVSSSHDPTILTW 544
 DB 443 SGAYNGKIKVMDLVAALDPRAAGTLCRTVYHSGRVPRLOPDEFQVSSSHDPTILTW 502
 QY 545 DEIANDPAQAEBPSPSPRTTYTISR 569
 DB 503 DEIANDPAQAEBPSPSPRTTYTISR 527
 RESULT 13
 ID 07ZVZ1 PRELIMINARY; PRT: 527 AA.
 AC 07ZVZ1;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)
 DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
 DE F-box and WD-40 domain protein 1B.
 GN Name=fboxwb;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maier M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -i- SIMILARITY: Contains 7 WD repeats.
 DR EMBL, BC045356; AAH45356.1; -

DR HSSP; Q9Y297; 1P22.
 DR ZFIN; ZDB-GENE-030131-6305; fbxwlb.
 DR InterPro; IPR001810; F-box.
 DR InterPro; IPR01680; WD40.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR Prodom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 527 AA; 60365 MW; 8AB60CEBB84963DA CRC64;

Query Match 74.2%; Score 2250; DB 2; Length 527;
 Best Local Similarity 75.0%; Pred. No. 8e-161;
 Matches 427; Conservative 49; Mismatches 51; Indels 42; Gaps 5;

QY 1 MDPBAVLQERALKFMNSEREDCNNGEPKRIPEKNSLRQYNSCARLCLNDETVCLA 60
 DB 1 MDPDK---EDKTLBELMNTGMESQINTD---EVSPKTTV----- 34

QY 61 STAMTEHCVAKTAKLANGTSSMIVPKORKLSASYKEKELCVKTFEOMSESDQVEFVHL 120
 DB 35 -----FKLGNG--SLAGSRKRPSSQSPKEXDLCQLPDOMSESQVEFVHL 80

QY 121 ISOMCHYOHGHNSTLYKPMLOQDFITLAPARGLDHIAENILSYDAKSLCAELVCCKEMY 180
 DB 81 IARMKHYOHGHNSTLYKPMLOQDFITLAPARGLDHIAENILSYDAKSLCAELVCCKEMY 140

QY 181 RYTSQGLMKKLIEMVVRTSLMRLAERKMGQYLFPKKPPDGNAPNSFYRALYPKII 240
 DB 141 RYISQGLMKKLIEMVVRTSLMRLAERKMGQYLFPKKPPDGNAPNSFYRALYPKII 198

QY 241 ODIEETIESNNRCGRSLQRIHCRSTSKGVYCLQYDDOKIVSGGLADNTIKIWDKNTLECK 300
 DB 199 ODIEETIESNNRCGRSLQRIHCRSTSKGVYCLQYDDOKIVSGGLADNTIKIWDKNTLECK 258

QY 301 RILHTGTSVLCLODERVIITGSSDSTYRVMDVNTGEMLNTLIHCEAVLHLPNNGM 360
 DB 259 KVLHTGTSVLCLODERVIITGSSDSTYRVMDVNTGEMLNTLIHCEAVLHLPNNGM 318

QY 361 VTCSKORSIAVWDMASPTDITLRVLYVGHRAAVNVVDFDKXIVASAGDRTIKVNTSTC 420
 DB 319 VTCSKORSIAVWDMASPTDITLRVLYVGHRAAVNVVDFDKXIVASAGDRTIKVNTSTC 378

QY 421 EFWRLTLNGHKGIAICLQYRDRLVVGSSDNTIRLWDIEGACLRVLEGHELVRCIRFDN 480
 DB 379 EFWRLTLNGHKGIAICLQYRDRLVVGSSDNTIRLWDIEGACLRVLEGHELVRCIRFDN 438

QY 481 KRIVGAYDGKIKVMDLVVAALDPRAPAGTLCLRTVEHSGRVRLOPDEFQIVSSSHDT 540
 DB 439 KRIVGAYDGKIKVMDLVVAALDPRAPAGTLCLRTVEHSGRVRLOPDEFQIVSSSHDT 498

QY 541 ILIWDPLNDPAQAEPSPSRRTYTYISR 569
 DB 499 ILIWDPLNVSSNGQSDGRSPSRRTYTYISR 527

RESULT 14
 Q86SD3 PRELIMINARY; PRT; 621 AA.
 AC Q86SD3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Beta-transducin repeat-containing homologue protein.
 GN Name=C1-betaTACP;
 OS Ciona intestinalis.

OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Cloniidae; Ciona.
 OK NCBI_TaxID=7719;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hotta K., Takahashi H., Satoh N.,
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 7 WD repeats.
 DR EMBL; AB076993; BACS7516.1; -.
 DR HSSP; Q9Y297; 1P22.
 DR InterPro; IPR01810; F-box.
 DR InterPro; IPR01680; WD40.
 DR InterPro; IPR01046; WD40_like.
 DR Pfam; PF00646; F-box; 1.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINRPT.
 DR Prodom; PD000018; WD40; 4.
 DR SMART; SM00256; FBOX; 1.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS50181; FBOX; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 5.
 DR PROSITE; PS50082; WD_REPEATS_2; 7.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 621 AA; 70791 MW; 6D176B121959F8C3 CRC64;

Query Match 70.1%; Score 2128; DB 2; Length 621;
 Best Local Similarity 72.6%; Pred. No. 1.5e-151;
 Matches 394; Conservative 63; Mismatches 68; Indels 18; Gaps 3;

QY 33 IIPKNSLRQYNSCARLCLNDETVCLASTAMKTENCVAKTAKLANGTSSMIVPKORK-- 89
 DB 91 ILPSHNIQS-----QDRIDVRNNTLDSGLPLTNDTNNPAQTVLSPRLKLSQ 140

QY 90 ---LSASYEKEKELCVKTFEOMSESDQVEFVHLISOMCHYOHGHNSTLYKPMLOQDFIT 146
 DB 141 QLSISEYKNERDSCFTGFTWSEQOVDVEFVHLILMCHYOHQINCLFLKPMLOQDFIS 200

QY 147 ALPARGLDHIAENILSYDAKSLCAELVCCKEMRYVSDGLMKKLIEMVVRTSLMRL 206
 DB 201 ALPARGLDHIAENILSYDAKSLCAELVCCKEMRYVSDGLMKKLIEMVVRTSLMRL 260

QY 207 AERGMGQYLPKNRPPGNAPNSFYRALYPKIIODIETIESNNRCGRSLQRIHCRSET 266
 DB 261 SERGMGQHLFKGRP--NSVPDSFRRSLYPSIISDIKEIESNNRCGRHDKRLMCSDN 318

QY 267 SKGVYCLQYDDOKIVSGGLADNTIKIWDKNTLECKRIITGHTGSVLCLODERVIITGSSD 326
 DB 319 SKGVYCLQYDDOKIVSGGLADNTIKIWDKNTLECKRIITGHTGSVLCLODERVIITGSSD 378

QY 327 STVAVMDVNTGEMLNTLIHCEAVLHLPNNGMVNTCSKORSIAVWDMASPTDITLRVLY 386
 DB 379 STVAVMDVNTGEMLNTLIHCEAVLHLPNNGMVNTCSKORSIAVWDMASPTDITLRVLY 438

QY 387 VGHRAAVNVVDFDKXIVASAGDRTIKVNTSTCEFWRLTLNGHKGIAICLQYRDRLVVG 446
 DB 439 VGHRAAVNVVDFDKXIVASAGDRTIKVNTLTCEFWRLTLNGHKGIAICLQYRDRLVVG 498

QY 447 SSDNTIRLWDIEGACLRVLEGHELVRCIRFDNKRIVSAGYDGKIKVMDLVVAALDPRAP 506
 DB 499 SSDNTIRLWDIEGACLRVLEGHELVRCIRFDNKRIVSAGYDGKIKVMDLVVAALDPRAP 558

QY 507 AGTCLRTVVEHSGRVRLOPDEFQIVSSSHDPTILLIWDPLNDPAQAEPSPSRRTYTY 566
 DB 559 SSTCLRTVVEHSGRVRLOPDEFQIVSSSHDPTILLIWDPLNDPAQAEPSPSRRTYTY 618

RESULT 15
 Q44382

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ID 044382 PRELIMINARY; PRT; 510 AA.
AC 044382;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE S1mb.
GN Name=S1mb; Synonyms=s1mb;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9812115; PubMed=9461217; DOI=10.1038/35154;
RA Jiang J., Struhl G.;
RT Regulation of the Hedgehog and Wntless signalling pathways by the F-
RT box/WD40-repeat protein S1mb."
RL Nature 391.493-496 (1998).
CC -1- SIMILARITY: Contains 7 WD repeats.
DR EMBL; AF032878; AAC38852.1; -.
DR HSSP; Q9Y297; 1P22.
DR Flybase; FBgn0023423; s1mb.
DR GO; GO:0019005; C:SCF ubiquitin ligase complex; NAS.
DR GO; GO:0045475; P:locomotor rhythm; IMP.
DR GO; GO:0030512; P:negative regulation of transforming growth . . .; NAS.
DR GO; GO:0030178; P:negative regulation of int receptor signal. . .; NAS.
DR GO; GO:0008590; P:regulation of frizzled signaling pathway; IMP.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; TAS.
DR GO; GO:0008589; P:regulation of smoothened receptor signaling. . .; IMP.
DR GO; GO:0008588; P:release of cytoplasmic sequestered NF-kappaB; IMP.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR InterPro; IPR011046; WD40_like.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00400; WD40; 7.
DR PRINTS; PR00320; GPROTEINRPT.
DR ProDom; PD000018; WD40; 4.
DR SMART; SM00256; PROX; 1.
DR SMART; SM00320; WD40; 7.
DR PROSITE; PS00678; WD_REPEATS_1; 5.
DR PROSITE; PS50082; WD_REPEATS_2; 7.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 510 AA; 58952 MW; DBB0243D3730A5E8 CRC64;

Query Match 68.9%; Score 2089.5; DB 2; Length 510;
Best Local Similarity 78.3%; Pred. No. 9.3e-149;
Matches 394; Conservative 48; Mismatches 54; Indels 7; Gaps 4;

QY 64 MTEKNCVAKTKLANG---TSSMIVPKQRLSAS--YEKKELCVKYFEQMSRSSDOVEPYE 118
DB 4 METDKIMEETN-SNAQAFITTMLYDFVRKDDSPYOTEREELCFQYFTQMSSEGVDFVE 62

QY 119 HLI SQMCHYOHGHINSYLPMLQORDFITLPAAGLDHIAENITLSYLDASLCAELVCKE 178
DB 63 HLLSMCHYOHGHQINAYLKPMLQORDFITLPIKGLDHIGENITLSYLDASLSSELVCKE 122

QY 179 WYRVTS DGLMKKLLIERMVRTDSLWRGLAERRGWCQYLFPKNKPPDGNAPNPSFYALYPK 238
DB 123 WLRVISEGLMKKLLIERKVRTDSLWRGLAERRMMQYLFKPRPGQ-TQRPHSFHRELFPK 181

QY 239 I IODIETESNWRGCRHSIORHCRSEFSKGYVCLQYDOKIVSGLRDNTIKIMDKNTLE 298
DB 182 I MNDIDSLENNWRGCRHMLRINCRSENSKGYVCLQYDOKIVSGLRDNTIKIMDRDTLQ 241

QY 299 CKRIITGHTGTYLCLQYDERVIITGSSDSTVAVMDVTGEMLNTLIHCEAVLHLRFNNG 358
DB 242 CVKTLMGHTGTYLCLQYDOKVIISGSSDSTVAVMDVTGEMVNTLIHCEAVLHLRFNNG 301

QY 359 MMVTCSKORSIAVMDMASPTDITLRRVLVGRRAVAVNVDFDDKYIVSASGDRITIKVWNTS 418
DB 302 MMVTCSKORSIAVMDMTSPSEITLRRVLVGRRAVAVNVDFDDKYIVSASGDRITIKWNTS 361
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QY 419 TCEPVRTLNGHKGRIACIQYRDRLVVGSSSDNTIRLMDIEGACLRVLEGHELVRCIRF 478
DB 362 TCEPVRTLNGHKGRIACIQYRDRLVVGSSSDNSITLMDIEGACLRVLEGHELVRCIRF 421
QY 479 DNKRIVSGAYDGKIKVMDLVVALDPRAPAGTLCRTLVESHSGVRRLQDFEQIVSSSHD 538
DB 422 DTKRIVSGAYDGKIKVMDLVVALDPRASNTLCNTLVHETGRVFRLLQDFEQIVSSSHD 481
QY 539 DTILWDFLNDPRAQAEPSPS 561
DB 482 DTILWDFLNDPRAQAEPSPS 504
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